

NYLLACTOSE- BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (N  
LBH) (FLAGELLAR SHEATH ADHESIN) (ADHESIN A) (FRAGMENT).//0.93:74:33//HEL  
ICOBACTER ACINONYX.//Q47947

F-PLACE1004425//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.81:70:42//HO  
MO SAPIENS (HUMAN).//P39195

F-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.9e-31:203:39//RA  
TTUS NORVEGICUS (RAT).//Q63448

F-PLACE1004437//ISOCITRATE DEHYDROGENASE [NAD] , MITOCHONDRIAL SUBUNIT BE  
TA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH  
) (FRAGMENT).//4.2e-93:140:100//MACACA FASCICULARIS (CRAB EATING MACAQUE  
) (CYNOMOLGUS MONKEY).//Q28479

F-PLACE1004451//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00013:40:62//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0066:218:23//DROSOPHILA MELAN  
OGASTER (FRUIT FLY).//P25823

F-PLACE1004467//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//7.8e-10:33:87//  
HOMO SAPIENS (HUMAN).//P39193

F-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e  
-56:92:58//HOMO SAPIENS (HUMAN).//P51522

F-PLACE1004473//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I.//  
0.019:136:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844

F-PLACE1004491//LYSIS PROTEIN.//0.95:53:30//BACTERIOPHAGE FR.//P19903

F-PLACE1004506//AUTOIMMUNOGENIC CANCER/TESTIS ANTIGEN NY-ESO-1 (LAGE-1).  
//0.58:66:34//HOMO SAPIENS (HUMAN).//P78358

F-PLACE1004510//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TA  
FII-150) (TAFII150).//3.0e-07:63:46//DROSOPHILA MELANOGASTER (FRUIT FLY)  
.//Q24325

F-PLACE1004516//HYPOTHETICAL PROTEIN 5' TO ASP-RICH AND HIS-RICH PROTEIN  
S (FRAGMENT).//0.95:62:29//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGA

L).//P14587

F-PLACE1004518//METALLOTHIONEIN 10-III (MT-10-III).//0.91:28:42//MYTILUS EDULIS (BLUE MUSSEL).//P80248

F-PLACE1004548//DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT.//0.94:75:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P19518

F-PLACE1004550//CUTICLE COLLAGEN 2.//0.90:155:31//CAENORHABDITIS ELEGANS .//P17656

F-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//3.2e-70:121:100//BOS TAURUS (BOVINE).//Q10568

F-PLACE1004629//PROTEIN OS-9 PRECURSOR.//1.7e-10:132:36//HOMO SAPIENS (HUMAN).//Q13438

F-PLACE1004645//TRANSCRIPTION INITIATION FACTOR IIB HOMOLOG (TFIIB).//0.0036:100:30//PYROCOCCUS FURIOSUS.//Q51731

F-PLACE1004646//PROBABLE UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9).//0.91:58:29//KLEBSIELLA PNEUMONIAE.//Q48481

F-PLACE1004658//GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 4 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2D) (NR2D) (NMDAR2D).//0.031:134:32 //MUS MUSCULUS (MOUSE).//Q03391

F-PLACE1004664//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION.//0.025:125:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781

F-PLACE1004672//HYPOTHETICAL 36.7 KD PROTEIN C2F7.14C IN CHROMOSOME I.//7.6e-52:158:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09704

F-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.4e-88:144:93//MUS MUSCULUS (MOUSE).//P12815

F-PLACE1004681//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.0e-34:70:100//MUS MUSCULUS (MOUSE).//Q60809

F-PLACE1004686//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.4e-08:48:62/

/HOMO SAPIENS (HUMAN).//P39192

F-PLACE1004691//METALLOTHIONEIN (MT).//0.064:24:45//ARIANTA ARBUSTORUM.//  
/P55946

F-PLACE1004693

F-PLACE1004716//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:27:37//  
PAN PANISCUS (PYGMY CHIMPANZEE) (BONOBO).//Q35587

F-PLACE1004722//HYPOTHETICAL 61.5 KD PROTEIN IN CLA4-MID1 INTERGENIC REG  
ION.//0.95:53:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48565

F-PLACE1004736//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22.//0.014:163:30//  
● RATTUS NORVEGICUS (RAT).//Q05175

F-PLACE1004740//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.9e-09:37:70/  
/HOMO SAPIENS (HUMAN).//P39194

F-PLACE1004743//HYPOTHETICAL 12.6 KD PROTEIN IN ALGR3 3' REGION.//0.99:72  
:33//PSEUDOMONAS AERUGINOSA.//P21484

F-PLACE1004751//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIA  
LYLTRANSFERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERA  
SE) (ST3GALIII) (ALPHA 2,3-ST) (GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4  
).//2.2e-08:90:38//HOMO SAPIENS (HUMAN).//Q11206

F-PLACE1004773//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)./  
● /3.2e-25:233:32//HOMO SAPIENS (HUMAN).//P16157

F-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAE  
RIN).//8.1e-26:210:30//RATTUS NORVEGICUS (RAT).//P30337

F-PLACE1004793//ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTE  
IN GP36].//0.00062:106:25//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6).//P102  
59

F-PLACE1004804

F-PLACE1004813//HYPOTHETICAL PROTEIN UL12.//1.0:22:40//HUMAN CYTOMEGALOV  
IRUS (STRAIN AD169).//P16777

F-PLACE1004814//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//

2.8e-06:136:25//CAENORHABDITIS ELEGANS.//Q09217

F-PLACE1004815

F-PLACE1004824//HYPOTHETICAL 106.7 KD PROTEIN IN MUP1-SPR3 INTERGENIC REGION.//2.3e-09:70:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53236

F-PLACE1004827//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3' REGION (ORF3).//0.

54:25:56//BACILLUS LICHENIFORMIS.//P22754

F-PLACE1004836//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.0066:12:66//BOS TAU RUS (BOVINE).//P20072

F-PLACE1004838

F-PLACE1004840

F-PLACE1004868//MALE STERILITY PROTEIN 2.//4.0e-16:172:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891

F-PLACE1004885

F-PLACE1004900//MAST CELL DEGRANULATING PEPTIDE PRECURSOR (MCDP) (MCD) (PEPTIDE 401).//1.0:23:47//APIS MELLIFERA (HONEYBEE).//P01499

F-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//7.3e-15:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//042643

F-PLACE1004913//HYPOTHETICAL 7.2 KD PROTEIN IN BCSA-DEGR INTERGENIC REGION.//1.0:42:33//BACILLUS SUBTILIS.//P54165

F-PLACE1004918//HYPOTHETICAL 12.4 KD PROTEIN IN RPS21B-MRS3 INTERGENIC REGION.//0.98:50:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47012

F-PLACE1004930//HYPOTHETICAL PROTEIN MJ0562.//0.82:44:36//METHANOCOCCUS JANNASCHII.//Q57982

F-PLACE1004934

F-PLACE1004937//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I.//9.0e-10:87:33//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053

F-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//4

.0e-14:184:25//CAENORHABDITIS ELEGANS.//Q11073

F-PLACE1004972//BROMELAIN INHIBITOR 2 (BI-II) (BROMELAIN INHIBITOR VI) (BI-VI).//1.0:35:37//ANANAS COMOSUS (PINEAPPLE).//P27478

F-PLACE1004979//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//5.3e-30:55:72//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1004982//M PROTEIN, SEROTYPE 12 PRECURSOR (FRAGMENT).//0.00049:124:27//STREPTOCOCCUS PYOGENES.//P19401

F-PLACE1004985//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:26:34//LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942

F-PLACE1005026//TELOMERE-BINDING PROTEIN HOMOLOG.//0.0011:179:27//EUPLOTES CRASSUS.//Q06183

F-PLACE1005027

F-PLACE1005046//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.082:44:36//BOS TAURUS (BOVINE).//P20072

F-PLACE1005052//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.38:36:44//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-PLACE1005055

F-PLACE1005066//RING CANAL PROTEIN (KELCH PROTEIN).//2.9e-38:194:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-PLACE1005077

F-PLACE1005085//INSECT TOXIN 1 (BOT IT1).//0.85:36:33//BUTHUS OCCITANUS TUNETANUS (COMMON EUROPEAN SCORPION).//P55902

F-PLACE1005086//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//8.5e-38:93:76//HOMO SAPIENS (HUMAN).//P39194

F-PLACE1005101//HYPOTHETICAL PROTEIN ZAP128 (FRAGMENT).//1.6e-11:35:100//HOMO SAPIENS (HUMAN).//P49753

F-PLACE1005102//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//3.0e-14:110:38//MUS MUSCULUS (MOUSE).//Q60821

F-PLACE1005108//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.41:35:34//BOS TAURUS (BOVINE).//P37359

F-PLACE1005111//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) (CHARGERIN II).//1.0:29:41//RATTUS NORVEGICUS (RAT).//P11608

F-PLACE1005128//RABPHILIN-3A (FRAGMENT).//5.9e-05:95:36//MUS MUSCULUS (MOUSE).//P47708

F-PLACE1005146//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 15 (FIN15).//0.17:48:35//MUS MUSCULUS (MOUSE).//Q61075

F-PLACE1005162//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.0e-31:60:76//HOMO SAPIENS (HUMAN).//P39189

F-PLACE1005176

F-PLACE1005181//HYPOTHETICAL 7 KD PROTEIN.//1.0:31:45//MEASLES VIRUS (STRAIN HALLE) (SUBACUTE SCLEROSE PANENCEPHALITIS VIRUS).//P06831

F-PLACE1005187//GLUCAN SYNTHASE-1 (EC 2.4.1.34) (1,3-BETA-GLUCAN SYNTHASE) (UDP-GLUCOSE-1,3-BETA-D-GLUCAN GLUCOSYLTRANSFERASE).//0.0025:58:34//EUROSPORA CRASSA.//P38678

F-PLACE1005206//HYPOTHETICAL 10.7 KD PROTEIN.//0.34:57:42//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20511

F-PLACE1005232//AMELOGENIN, Y ISOFORM PRECURSOR.//0.70:60:35//HOMO SAPIENS (HUMAN).//Q99218

F-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//0.0017:114:27//PHYCOMYCES BLAKESLEEEANUS.//Q01577

F-PLACE1005261//HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II.//1.2e-38:206:41//CAENORHABDITIS ELEGANS.//Q10003

F-PLACE1005266

F-PLACE1005277//PROTEIN GURKEN PRECURSOR.//0.58:95:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P42287

F-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.0e-12:211:29//GALLUS GALLUS (CHICKEN).//P53352

F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.8e-78:205:78//BOS TAURUS (BOVINE).//P08760

F-PLACE1005308//WOUND-INDUCED BASIC PROTEIN.//0.99:40:40//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).//Q09020

F-PLACE1005313//HYPOTHETICAL 8.7 KD PROTEIN IN LEUX-FECE INTERGENIC REGION (067).//0.15:36:41//ESCHERICHIA COLI.//P39355

F-PLACE1005327//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//1.0:19:52//HOMO SAPIENS (HUMAN).//P30808

F-PLACE1005331//BREAKPOINT CLUSTER REGION PROTEIN.//0.00021:98:35//HOMO SAPIENS (HUMAN).//P11274

F-PLACE1005335//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-3.//0.37:98:33//MUS MUSCULUS (MOUSE).//P81067

F-PLACE1005373//PSEUDOURIDYLATE SYNTHASE 4 (EC 4.2.1.70) (PSEUDOURIDINE SYNTHASE 4) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//0.010:96:28//SACCHAROMYCES CERESIAE (BAKER'S YEAST).//P48567

F-PLACE1005374

F-PLACE1005409

F-PLACE1005453//LICHENASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE).//1.0:50:32//NICOTIANA PLUMBAGINIFOLIA (LEADWORT-LEAVED TOBACCO).//P07979

F-PLACE1005467//KERATIN, FEATHER (F-KER).//0.0095:42:35//LARUS NOVAE-HOLANDIAE (SILVER GULL).//P02451

F-PLACE1005471//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.23:49:32//PHYTOPHTHORA INFESTANS (POTATO LATE BLIGHT FUNGUS).//Q37598

F-PLACE1005477//HYPOTHETICAL PROTEIN ORF-1137.//9.6e-13:115:38//MUS MUSCULUS (MOUSE).//P11260

F-PLACE1005480//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.97:33:30//HORDEUM VULGARE (BARLEY).//P17991

F-PLACE1005481//HUNCHBACK PROTEIN (FRAGMENT).//0.30:52:38//APIS MELLIFER  
A (HONEYBEE).//P31504

F-PLACE1005494//TRANSIENT-RECEPTOR-POTENTIAL PROTEIN.//3.9e-05:87:33//DR  
OSOPHILA MELANOGASTER (FRUIT FLY).//P19334

F-PLACE1005502

F-PLACE1005526//IMMEDIATE-EARLY PROTEIN IE180.//4.6e-05:132:32//PSEUDORA  
BIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-PLACE1005528//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//3.4e-09:31:74/  
/HOMO SAPIENS (HUMAN).//P39195

F-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.  
//9.7e-50:148:58//CAENORHABDITIS ELEGANS.//Q09251

F-PLACE1005550//HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III./  
/3.0e-21:127:37//CAENORHABDITIS ELEGANS.//P34524

F-PLACE1005554//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT).//0.84:38:31//DIPLO  
DOMYS CALIFORNICUS (KANGAROO RAT).//P16359

F-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//4.8e-09:60:48//CRYPTOCOCCUS  
NEOFORMANS (FILOBASIDIUM NEOFORMANS).//P46288

F-PLACE1005574//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.89:44:29/  
/BOS TAURUS (BOVINE).//P03929

F-PLACE1005584//MALE SPECIFIC SPERM PROTEIN MST87F.//0.00030:33:48//DROS  
OPHILA MELANOGASTER (FRUIT FLY).//P08175

F-PLACE1005595//IMMEDIATE-EARLY PROTEIN IE180.//0.00048:162:30//PSEUDORA  
BIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-PLACE1005603//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROT  
EIN).//0.00034:83:30//TETRAHYMENA PYRIFORMIS.//P40625

F-PLACE1005611//DNAJ PROTEIN.//8.6e-20:108:48//CLOSTRIDIUM ACETOBUTYLICU  
M.//P30725

F-PLACE1005623//EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1.-) (ER  
K5) (ERK4) (BMK1 KINASE).//0.80:116:31//HOMO SAPIENS (HUMAN).//Q13164

F-PLACE1005630//INTERLEUKIN-14 PRECURSOR (IL-14) (HIGH MOLECULAR WEIGHT B-CELL GROWTH FACTOR) (HMW-BCGF).//0.0024:74:39//HOMO SAPIENS (HUMAN).//P40222

F-PLACE1005639//EXTRACELLULAR MATRIX PROTEIN 1 (SECRETORY COMPONENT P85) (FRAGMENT).//0.72:18:61//RATTUS NORVEGICUS (RAT).//Q62894

F-PLACE1005646//RNA HELICASE-LIKE PROTEIN DB10.//4.8e-29:172:45//NICOTIANA SYLVESTRIS (WOOD TOBACCO).//P46942

F-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//3.7e-64:133:75//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//Q60561

F-PLACE1005666//CHLOROPLAST 50S RIBOSOMAL PROTEIN L28.//0.57:36:41//PORPHYRA PURPUREA.//P51224

F-PLACE1005698//HYPOTHETICAL PROTEIN IN SIGD 3' REGION (ORFC) (FRAGMENT).//0.50:61:29//BACILLUS SUBTILIS.//P40405

F-PLACE1005727//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).//0.46:27:51//BRASSICA NAPUS (RAPE).//P40603

F-PLACE1005730//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//0.95:21:52//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456

F-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11.//3.4e-46:111:53//MUS MUSCULUS (MOUSE).//Q60710

F-PLACE1005755//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REGION.//2.6e-12:66:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42951

F-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//1.5e-26:69:57//RATTUS NORVEGICUS (RAT).//P08635

F-PLACE1005799//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.028:96:32//HOMO SAPIENS (HUMAN).//P26371

F-PLACE1005802//PROTEIN PROSPERO.//0.86:64:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//P29617

F-PLACE1005803//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.

//1.0:95:25//MUS MUSCULUS (MOUSE).//P17564

F-PLACE1005804//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//2.8e-73:198:73//MUS MUSCULUS (MOUSE).//P39098

F-PLACE1005813//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION.//0.022:78:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057

F-PLACE1005828//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.8e-23:56:76//HOMO SAPIENS (HUMAN).//P39195

F-PLACE1005834//LATE CONTROL GENE B PROTEIN (GPB).//0.97:33:39//BACTERIOPHAGE 186.//P08711

F-PLACE1005845

F-PLACE1005850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//5.5e-28:96:73//HOMO SAPIENS (HUMAN).//P39194

F-PLACE1005851

F-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//2.2e-99:155:95//BOS TAURUS (BOVINE).//Q10568

F-PLACE1005884

F-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//1.8e-33:137:49//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P54069

F-PLACE1005898//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MLRQ) (CI-MLRQ).//0.77:58:34//HOMO SAPIENS (HUMAN).//Q00483

F-PLACE1005921//AIG1 PROTEIN.//1.4e-23:165:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P54120

F-PLACE1005923//HYPOTHETICAL 22.4 KD PROTEIN (ORF16).//0.90:118:28//PARAMECIUM TETRAURELIA.//P15617

F-PLACE1005925//HYPOTHETICAL GENE 30 PROTEIN.//0.94:57:29//HERPESVIRUS SAIMIRI (STRAIN 11).//Q01010

F-PLACE1005932//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.42:128:32//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-PLACE1005934//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.40:76:35//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414

F-PLACE1005936//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.50:15:66//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CLONE 12) (HIV-1).//P04326

F-PLACE1005951//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.0025:135:32//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-PLACE1005953//HIGH POTENTIAL IRON-SULFUR PROTEIN (HIPIP).//0.64:57:33//RHODOFERAX FERMENTANS.//P80882

F-PLACE1005955//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//1.0e-32:110:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821

F-PLACE1005966//TACHYPLESIN II PRECURSOR.//0.97:31:35//TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB).//P14214

F-PLACE1005968//GATA FACTOR SREP.//0.17:52:40//PENICILLIUM CHRYSOGENUM.//Q92259

F-PLACE1005990//CELL PATTERN FORMATION-ASSOCIATED PROTEIN.//0.36:55:36//EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).//P36011

F-PLACE1006002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.5e-36:102:75//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1006003//HYPOTHETICAL 6.8 KD PROTEIN IN COX3-NAD1 INTERGENIC REGION (ORF 61).//1.0:22:40//MARCHANTIA POLYMORPHA (LIVERWORT).//P38473

F-PLACE1006011//POLY [ADP-RIBOSE] POLYMERASE (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP- RIBOSYLTRANSFERASE) (POLY [ADP-RIBOSE] SYNTHETASE).//2.8e-21:163:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q11207

F-PLACE1006017//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.1e-10:43:67//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1006037//VITELLOGENIN I PRECURSOR (VTG I) [CONTAINS: LIPOVITELLIN

1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2)].//0.00019:123:37//FUNDULUS HETEROCLITUS (KILLIFISH) (MUMMICHOGL).//Q90508

F-PLACE1006040//CAMP-REGULATED PHOSPHOPROTEIN 19 (ARPP-19).//3.2e-40:110:76//HOMO SAPIENS (HUMAN).//P56211

F-PLACE1006076//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR A-II.//0.99:30:40//ARACHIS HYPOGAEA (PEANUT).//P01066

F-PLACE1006119//IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT) (RNA-BINDING PROTEIN 5).//8.8e-94:218:76//HOMO SAPIENS (HUMAN).//000410

F-PLACE1006129//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.00092:228:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

F-PLACE1006139//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//5.9e-55:128:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P436

16

F-PLACE1006143//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.4e-25:107:63//HOMO SAPIENS (HUMAN).//P39194

F-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//1.3e-21:168:32//SUS SCROFA (PIG).//P98110

F-PLACE1006159//COLD SHOCK INDUCED PROTEIN TIR1 PRECURSOR (SERINE-RICH PROTEIN 1).//0.46:98:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P1086

3

F-PLACE1006164//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.70:28:42//ARTEMIA SALINA (BRINE SHRIMP).//P19049

F-PLACE1006167//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.9e-05:167:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTER HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.1e-67:157:88//MUS MUSCULUS (MO

USE).//P17427

F-PLACE1006187//G1/S-SPECIFIC CYCLIN E.//5.6e-75:224:62//HOMO SAPIENS (HUMAN).//P24864

F-PLACE1006195//T-RELATED PROTEIN (TRP) (BRACHYENTERON PROTEIN).//0.99:1  
77:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P55965

F-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.0e-33:1  
83:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747

F-PLACE1006205

F-PLACE1006223//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.0001  
5:22:50//MUS MUSCULUS (MOUSE).//P15265

F-PLACE1006225//VIRION INFECTIVITY FACTOR (SOR PROTEIN).//1.0:63:34//HUMAN  
IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18805

F-PLACE1006236

F-PLACE1006239//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT).//0.48:23:52/  
/ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P51407

F-PLACE1006246//CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR).//0.012:84:30//  
MUS MUSCULUS (MOUSE).//Q61420

F-PLACE1006248//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//0.017:203:22  
//RATTUS NORVEGICUS (RAT).//P41777

F-PLACE1006262//L-FUCULOSE PHOSPHATE ALDOLASE (EC 4.1.2.17).//0.84:25:52  
//HAEMOPHILUS INFLUENZAE.//P44777

F-PLACE1006288

F-PLACE1006318//CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 (AFP1) (M1).//1.0:29:  
48//SINAPIS ALBA (WHITE MUSTARD) (BRASSICA HIRTA).//P30231

F-PLACE1006325//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT K  
INASE INHIBITOR P57) (P57KIP2).//0.99:97:32//HOMO SAPIENS (HUMAN).//P499

18

F-PLACE1006335//PROLINE-RICH PEPTIDE P-B.//0.56:19:52//HOMO SAPIENS (HUMAN).//P02814

F-PLACE1006357

F-PLACE1006360

F-PLACE1006368//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//  
/0.0057:122:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32380

F-PLACE1006371//ARS BINDING PROTEIN 1.//0.00030:142:30//SCHIZOSACCHAROMY  
CES POMBE (FISSION YEAST).//P49777

F-PLACE1006382//NEUROTOXIN V.//0.85:28:39//ANDROCTONUS MAURETANICUS MAUR  
ETANICUS (SCORPION).//P01482

F-PLACE1006385//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REG  
ION.//3.1e-35:165:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160

F-PLACE1006412//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.3e-08:40:47//HO  
MO SAPIENS (HUMAN).//P08547

F-PLACE1006414//FORKHEAD-RELATED TRANSCRIPTION FACTOR 4 (FREAC-4).//3.8e  
-05:123:39//HOMO SAPIENS (HUMAN).//Q16676

F-PLACE1006438//ZINC FINGER PROTEIN 165.//2.8e-21:76:64//HOMO SAPIENS (H  
UMAN).//P49910

F-PLACE1006445//SUPPRESSOR OF HAIRY WING PROTEIN.//0.058:99:29//DROSOPHI  
LA VIRILIS (FRUIT FLY).//Q08876

F-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA  
LIGASE) (ACYL- ACTIVATING ENZYME).//1.8e-64:177:50//ESCHERICHIA COLI.//P  
27550

F-PLACE1006470

F-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//2.0e-47:120:85//GALLUS GALLU  
S (CHICKEN).//Q90595

F-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.8e  
-85:173:95//CANIS FAMILIARIS (DOG).//Q00004

F-PLACE1006492//VERY HYPOTHETICAL 11.2 KD PROTEIN C56F8.13 IN CHROMOSOME  
I.//0.75:32:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10261

F-PLACE1006506

F-PLACE1006521

F-PLACE1006531//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.  
//1.3e-53:167:61//CAENORHABDITIS ELEGANS./P34681

F-PLACE1006534

F-PLACE1006540

F-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.3e-07:242:2  
3//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922  
F-PLACE1006598//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!//0.17:43:51//H  
OMO SAPIENS (HUMAN).//P39190

F-PLACE1006615//ACROSIN PRECURSOR (EC 3.4.21.10).//3.6e-05:66:43//ORYCTO  
LAGUS CUNICULUS (RABBIT).//P48038

F-PLACE1006617//HYPOTHETICAL 14.6 KD PROTEIN (READING FRAME C) (REPLICAT  
ION).//1.0:74:29//STAPHYLOCOCCUS AUREUS.//P03861

F-PLACE1006626//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//2.9e-1  
0:73:46//CAENORHABDITIS ELEGANS./P34529

F-PLACE1006629//HYPOTHETICAL PROTEIN BB0410.//1.0:23:43//BORRELIA BURGDO  
RFERI (LYME DISEASE SPIROCHETE).//051371

F-PLACE1006640

F-PLACE1006673

F-PLACE1006678//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYCTO  
LAGUS CUNICULUS (RABBIT).//P02456

F-PLACE1006704//BROAD-COMPLEX CORE-TNT1-Q1-Z1 PROTEIN (BRCORE-TNT1-Q1-Z1  
) [CONTAINS: BROAD-COMPLEX CORE-Q1-Z1 PROTEIN].//0.00062:157:26//DROSOPH  
ILA MELANOGASTER (FRUIT FLY).//Q01295

F-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADEN  
YLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//  
1.3e-07:127:36//CORYNEBACTERIUM AMMONIAGENES (BREVIBACTERIUM AMMONIAGENE  
S).//Q59263

F-PLACE1006754//CARCINOEMBRYONIC ANTIGEN CGM1 PRECURSOR (CD66D ANTIGEN).

//1.9e-19:78:53//HOMO SAPIENS (HUMAN).//P40198

F-PLACE1006760//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.21:107:30//RATTUS NORVEGICUS (RAT).//P13941

F-PLACE1006779//CYTOTOXIN 5 (CTX V).//1.0:20:30//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P25517

F-PLACE1006782//ZINC FINGER PROTEIN 1.//0.00052:178:28//CANDIDA ALBICANS (YEAST).//P28875

F-PLACE1006792

F-PLACE1006795//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAW (SHAW2).//1.0:80:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17972

F-PLACE1006800//HYPOTHETICAL 9.4 KD PROTEIN.//0.99:62:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20569

F-PLACE1006805

F-PLACE1006815//HYPOTHETICAL PROTEIN UL61.//0.038:146:32//HUMAN CYTOMEGA LOVIRUS (STRAIN AD169).//P16818

F-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-98:239:76//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//0.061:34:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50102

F-PLACE1006860

F-PLACE1006867

F-PLACE1006878//HYPOTHETICAL 8.2 KD PROTEIN IN MOBL 3' REGION (ORF 3).//0.85:27:37//THIOBACILLUS FERROOXIDANS.//P20087

F-PLACE1006883//VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).//0.78:51:37//MUS MUSCULUS (MOUSE).//P48281

F-PLACE1006901//HYPOTHETICAL 8.1 KD PROTEIN.//0.99:55:23//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20567

F-PLACE1006904//MATING-TYPE LOCUS ALLELE B1 PROTEIN.//0.95:86:26//USTILA  
GO MAYDIS (SMUT FUNGUS).//P22015

F-PLACE1006917//HYPOTHETICAL 40.9 KD PROTEIN C08B11.5 IN CHROMOSOME II.//  
/6.9e-15:101:45//CAENORHABDITIS ELEGANS.//Q09442

F-PLACE1006932//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.089:28:39/  
/HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251

F-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//  
0.93:35:48//CAENORHABDITIS ELEGANS.//Q10000

F-PLACE1006956//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TA  
FII-135) (TAFII135) (TAFII-130) (TAFII130).//0.00079:122:36//HOMO SAPIEN  
S (HUMAN).//000268

F-PLACE1006958//OSMOTIC STRESS PROTEIN 94 (HEAT SHOCK 70-RELATED PROTEIN  
APG-1).//8.8e-70:140:98//MUS MUSCULUS (MOUSE).//P48722

F-PLACE1006961

F-PLACE1006962//APOLIPOPROTEIN C-I PRECURSOR (APO-C1).//1.0:25:40//PAPIO  
HAMADRYAS (HAMADRYAS BABOON).//P34929

F-PLACE1006966//HYPOTHETICAL 49.1 KD PROTEIN IN SSB2-SPX18 INTERGENIC RE  
GION.//1.6e-47:221:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40160

F-PLACE1006989//HYPOTHETICAL 13.1 KD HIT-LIKE PROTEIN IN P37 5' REGION.//  
0.15:46:32//MYCOPLASMA HYORHINIS.//P32083

F-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PR  
OTEIN 12) (DER12).//3.4e-09:120:29//HOMO SAPIENS (HUMAN).//Q14542

F-PLACE1007021//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00046:42:59//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE1007045//HYPOTHETICAL PROTEIN ORF-1137.//8.1e-14:115:35//MUS MUSC  
ULUS (MOUSE).//P11260

F-PLACE1007053//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0  
38:48:39//HOMO SAPIENS (HUMAN).//P22531

F-PLACE1007068//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL

OXIDASE).//0.0040:113:39//GALLUS GALLUS (CHICKEN).//Q05063  
F-PLACE1007097//HYPOTHETICAL 6.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGIO  
N.//0.97:47:29//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNP  
V).//P41663  
F-PLACE1007105//HYPOTHETICAL 83.6 KD PROTEIN C15A10.10 IN CHROMOSOME I./  
/2.9e-33:219:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013730  
F-PLACE1007111  
F-PLACE1007112//HYPOTHETICAL 9.2 KD PROTEIN.//0.47:75:28//ESCHERICHIA CO  
LI.//P03853  
● F-PLACE1007132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.8e-11:56:57//  
HOMO SAPIENS (HUMAN).//P39188  
F-PLACE1007140//GAR2 PROTEIN.//0.72:185:24//SCHIZOSACCHAROMYCES POMBE (F  
ISSION YEAST).//P41891  
F-PLACE1007178//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C.//0.97:79:30//MYCO  
BACTERIUM TUBERCULOSIS.//Q10826  
F-PLACE1007226//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC REG  
ION (0378).//1.9e-15:123:32//ESCHERICHIA COLI.//P52062  
F-PLACE1007238//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL).//5.5e-10:  
98:44//ACANTHAMOEBA CASTELLANII (AMOEBA).//P19706  
● F-PLACE1007239//TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELON  
GATION FACTOR A).//3.9e-19:96:57//HOMO SAPIENS (HUMAN).//P23193  
F-PLACE1007242//GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM B  
(RALGEF).//1.0:132:30//RATTUS NORVEGICUS (RAT).//Q03386  
F-PLACE1007243//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REG  
ION.//0.041:114:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39981  
F-PLACE1007257//DIAPHANOUS PROTEIN.//1.3e-42:205:46//DROSOPHILA MELANOGA  
STER (FRUIT FLY).//P48608  
F-PLACE1007274//CADMIUM-METALLOTHIONEIN (CD-MT).//0.054:60:30//HELIX POM  
ATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187

F-PLACE1007276//BETA-DEFENSIN 1 PRECURSOR (RHBD-1) (DEFENSIN, BETA 1).//

1.0:42:28//SUS SCROFA (PIG).//062697

F-PLACE1007282//OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8].//0.070:126:27//HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST. THOMAS 3).//P11200

F-PLACE1007286

F-PLACE1007301//HYPOTHETICAL PROTEIN KIAA0168.//0.042:61:39//HOMO SAPIENS (HUMAN).//P50749

F-PLACE1007317

F-PLACE1007342//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//1.7e-06:77:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002

F-PLACE1007346//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A INTERACTING PROTEIN) (KRIP-1).//0.0026:147:27//MUS MUSCULUS (MOUSE).//Q62318

F-PLACE1007367//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.3e-37:110:76//HOMO SAPIENS (HUMAN).//P39189

F-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//4.7e-07:71:39//CAENORHABDITIS ELEGANS.//P27715

F-PLACE1007386//HYPOTHETICAL 7.6 KD PROTEIN IN FLO1-PHO11 INTERGENIC REGION.//0.74:48:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39561

F-PLACE1007402//TRANSCRIPTIONAL REGULATORY PROTEIN ENTR (ENTERICIDIN R).//0.99:63:36//CITROBACTER FREUNDII.//069280

F-PLACE1007409//WHITE PROTEIN.//7.9e-38:179:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P10090

F-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//0.031:159:23//HOMO SAPIENS (HUMAN).//P27487

F-PLACE1007450//ZINC FINGER PROTEIN 39 (ZINC FINGER PROTEIN KOX27) (FRAGMENT).//0.023:36:50//HOMO SAPIENS (HUMAN).//P17038

F-PLACE1007452//HYPOTHETICAL 22.1 KD PROTEIN IN CCP1-MET1 INTERGENIC REGION.//2.2e-18:85:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36149

F-PLACE1007454//PHOTOSYSTEM II REACTION CENTRE N PROTEIN.//0.66:13:53//CHLAMYDOMONAS REINHARDTII.//Q06480

F-PLACE1007460//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.93:45:33//SUS SCROFA (PIG).//Q35914

F-PLACE1007478//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//5.3e-08:50:56//MUS MUSCULUS (MOUSE).//P11369

F-PLACE1007484//HYPOTHETICAL 6.8 KD PROTEIN IN REPLICATION ORIGIN REGION.//0.87:43:37//ESCHERICHIA COLI.//P03849

F-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//1.2e-25:202:31//HOMO SAPIENS (HUMAN).//P98174

F-PLACE1007507//HYPOTHETICAL 16.0 KD PROTEIN IN TAF60-G4P1 INTERGENIC REGION.//0.12:128:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53139

F-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//2.1e-45:209:48//BOS TAURUS (BOVINE).//P08728

F-PLACE1007524//HYPOTHETICAL 9.2 KD PROTEIN.//0.74:80:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20550

F-PLACE1007525.

F-PLACE1007537//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.045:92:30//MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT).//P80144

F-PLACE1007544//IMMEDIATE-EARLY PROTEIN IE180.//1.5e-07:59:50//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.5e-16:188:34//CAENORHABDITIS ELEGANS.//P34537

F-PLACE1007557

F-PLACE1007583//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT).//0.98:72:33//DAUCUS CAROTA (CARROT).//P06600

F-PLACE1007598//ZINC FINGER PROTEIN 92 (ZINC FINGER PROTEIN HTF12) (FRAGMENT).//1.7e-11:88:43//HOMO SAPIENS (HUMAN).//Q03936

F-PLACE1007618//ANION EXCHANGE PROTEIN 2 (NON-ERYTHROID BAND 3-LIKE PROTEIN) (B3RP).//0.19:109:27//MUS MUSCULUS (MOUSE).//P13808

F-PLACE1007621//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT).//0.98:34:41//PSEUDOMONAS AERUGINOSA.//P23621

F-PLACE1007632//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//0.70:110:34//BOS TAURUS (BOVINE).//P02465

F-PLACE1007645//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:20:45//STRUTHIO CAMELUS (OSTRICH).//021401

F-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.1e-06:197:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-PLACE1007677//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.0:47:46//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//2.7e-06:116:28//AEDES ALBOPICTUS (FOREST DAY MOSQUITO).//Q26457

F-PLACE1007690//SPERM PROTAMINE P1.//0.12:26:50//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA).//P35311

F-PLACE1007697//SPERM PROTAMINE P1.//0.19:34:52//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305

F-PLACE1007705//BIOH PROTEIN.//0.015:97:29//ESCHERICHIA COLI.//P13001

F-PLACE1007706//HYPOTHETICAL 112.2 KD PROTEIN IN TIF35-NPL3 INTERGENIC REGION (ORF1).//5.3e-55:190:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32898

F-PLACE1007725

F-PLACE1007729//PROTEASE (EC 3.4.23.-).//1.8e-21:136:42//MOUSE MAMMARY T  
UMOR VIRUS (STRAIN BR6).//P10271

F-PLACE1007730//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.0031:7  
7:40//HOMO SAPIENS (HUMAN).//P81489

F-PLACE1007737//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.78:39:56//HO  
MO SAPIENS (HUMAN).//P39195

F-PLACE1007743

F-PLACE1007746//RRP5 PROTEIN HOMOLOG (KIAA0185) (FRAGMENT).//0.0066:168:  
25//HOMO SAPIENS (HUMAN).//Q14690

F-PLACE1007791//KRUEPPEL PROTEIN (FRAGMENT).//0.62:17:41//LITHOBius FORF  
ICATUS.//Q01872

F-PLACE1007807//HYPOTHETICAL 6.4 KD PROTEIN IN BLTR-SPOIIIC INTERGENIC R  
EGION.//1.0:40:30//BACILLUS SUBTILIS.//P54446

F-PLACE1007810//ANTHOPLEURIN A (TOXIN AP-A).//0.79:28:46//ANTHOPLURA XA  
NTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01530

F-PLACE1007829//SPORE COAT PROTEIN G.//1.0:65:38//BACILLUS SUBTILIS.//P3  
9801

F-PLACE1007843

F-PLACE1007846//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-32:37:94//HO  
MO SAPIENS (HUMAN).//P08547

F-PLACE1007852//RHO-RELATED GTP-BINDING PROTEIN RHOH (GTP-BINDING PROTEI  
N TTF).//8.7e-05:138:30//HOMO SAPIENS (HUMAN).//Q15669

F-PLACE1007858//ANAPHASE SPINDLE ELONGATION PROTEIN.//0.0039:127:25//SAC  
CHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50275

F-PLACE1007866

F-PLACE1007877

F-PLACE1007897//CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-  
1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHO

CYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (HAM1 ANTIGEN).//0.44:128:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//Q60522

F-PLACE1007908//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//5.5e-28:61:65//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1007946//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC.//0.84:48:37//PSEUDOMONAS AERUGINOSA.//P04139

F-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION.//0.00070:96:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38226

F-PLACE1007955//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II.//0.00027:255:23//CAENORHABDITIS ELEGANS.//Q09625

F-PLACE1007958//HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17).//1.7e-09:127:30//MUS MUSCULUS (MOUSE).//P70453

F-PLACE1007969//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//2.4e-05:104:37//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

F-PLACE1007990//SPERM PROTAMINE P1.//0.78:36:47//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLATYPUS).//P35307

F-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//1.2e-16:128:39//RATTUS NORVEGICUS (RAT).//Q63622

F-PLACE1008002

F-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105).//3.9e-106:208:93//RATTUS NORVEGICUS (RAT).//P52590

F-PLACE1008045//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//3.9e-09:49:53//BOS TAURUS (BOVINE).//P25508

F-PLACE1008080//RNA REPLICASE POLYPOLYPROTEIN (EC 2.7.7.48).//0.00025:100:27//EGGPLANT MOSAIC VIRUS.//P20126

F-PLACE1008095//PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4) (PPO).//0.90:74:  
25//MYCOBACTERIUM TUBERCULOSIS.//053230

F-PLACE1008111//HYPOTHETICAL PROTEIN MJECS12.//0.30:38:42//METHANOCOCCUS  
JANNASCHII.//Q60311

F-PLACE1008122//PEA2 PROTEIN (PPF2 PROTEIN).//0.0085:117:34//SACCHAROMYC  
ES CEREVISIAE (BAKER'S YEAST).//P40091

F-PLACE1008129//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//1.8  
e-06:154:36//GALLUS GALLUS (CHICKEN).//P02467

F-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.  
//1.4e-13:227:36//CAENORHABDITIS ELEGANS.//Q09531

F-PLACE1008177//TRICHOHYALIN.//2.7e-10:230:26//OVIS ARIES (SHEEP).//P227  
93

F-PLACE1008181

F-PLACE1008198//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.  
00044:121:34//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-PLACE1008201//ZINC FINGER PROTEIN ZFMSA12A.//3.0e-05:82:37//MICROPTERU  
S SALMOIDES (LARGEMOUTH BASS).//P38621

F-PLACE1008209//METALLOTHIONEIN-I (MT-I).//0.95:39:35//CERCOPITHECUS AET  
HIOPS (GREEN MONKEY) (GRIVET).//P02797

F-PLACE1008231//PROCYCLIC FORM SPECIFIC POLYPEPTIDE B1-ALPHA PRECURSOR (  
PROCYCLIN) (PARP).//0.028:23:52//TRYPANOSOMA BRUCEI BRUCEI.//P08469

F-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.2e-23:14  
8:38//PODOSPORA ANSERINA.//Q00808

F-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).  
//1.1e-97:222:81//BOS TAURUS (BOVINE).//P53620

F-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//5.8e-20:161:37//S  
ACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P12689

F-PLACE1008280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.1e-23:124:42//H  
OMO SAPIENS (HUMAN).//P08547

F-PLACE1008309//HYPOTHETICAL 98.3 KD PROTEIN C9G1.06C IN CHROMOSOME I.//  
0.47:99:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//014302

F-PLACE1008329//PUTATIVE Z PROTEIN.//0.73:52:28//OVIS ARIES (SHEEP).//P0  
8105

F-PLACE1008330//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.0e-37:75:81/  
/HOMO SAPIENS (HUMAN).//P39194

F-PLACE1008331//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.1e-08:70:50//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE1008356//FRUIT PROTEIN PKIWI501.//0.0037:148:29//ACTINIDIA CHINEN  
SIS (KIWI) (YANGTAO).//P43393

F-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//3.5e-18:205:30//DRO  
SOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-PLACE1008369

F-PLACE1008392

F-PLACE1008398//GENE 33 POLYPEPTIDE.//1.5e-102:225:84//RATTUS NORVEGICUS  
(RAT).//P05432

F-PLACE1008401//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.9e-08:186:34//M  
US MUSCULUS (MOUSE).//P05143

F-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS AS  
SOCIATED PROTEIN) (TAP).//9.4e-105:207:98//BOS TAURUS (BOVINE).//P41541

F-PLACE1008405

F-PLACE1008424//PROTEIN UL56.//1.0:65:33//HERPES SIMPLEX VIRUS (TYPE 1 /  
STRAIN HFEM).//P36297

F-PLACE1008426//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN  
II).//4.4e-05:185:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q99323

F-PLACE1008429//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22.//0.00054:172:25  
//RATTUS NORVEGICUS (RAT).//Q05175

F-PLACE1008437//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.  
//1.9e-23:226:34//CAENORHABDITIS ELEGANS.//P34681

F-PLACE1008455//DNA-BINDING PROTEIN (AGNOPROTEIN).//0.97:23:52//BUDGERIGAR FLEDGLING DISEASE VIRUS (BFDV).//P13893

F-PLACE1008457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.1e-12:89:47//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1008465//ZINC FINGER PROTEIN 31 (ZINC FINGER PROTEIN KOX29) (FRAGMENT).//0.00017:23:43//HOMO SAPIENS (HUMAN).//P17040

F-PLACE1008488//HYPOTHETICAL PROTEIN UL61.//9.1e-05:204:30//HUMAN CYTOME GALOVIRUS (STRAIN AD169).//P16818

F-PLACE1008524//HOMEobox PROTEIN HLX1 (HOMEobox PROTEIN HB24).//0.95:74:36//HOMO SAPIENS (HUMAN).//Q14774

F-PLACE1008531//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.1e-05:86:45//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1008532//HYPOTHETICAL 36.4 KD PROTEIN IN SMP1-MBA1 INTERGENIC REGION.//3.9e-21:62:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38298

F-PLACE1008533//HYPOTHETICAL 86.2 KD PROTEIN C4G8.04 IN CHROMOSOME I.//3.5e-06:118:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09830

F-PLACE1008568//NEURONATIN.//0.046:34:52//HOMO SAPIENS (HUMAN).//Q16517

F-PLACE1008584//HUNCHBACK PROTEIN (FRAGMENT).//0.94:30:43//LITHOBius FORficatus.//Q02030

F-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//3.9e-123:224:96//RATTUS NORVEGICUS (RAT).//P37199

F-PLACE1008621//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//5.0e-05:31:67//HOMO SAPIENS (HUMAN).//P20931

F-PLACE1008625//DISAGREGIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).//0.87:17:52//ORNITHODOROS MOUBATA (SOFT TICK).//P36235

F-PLACE1008626//METALLOTHIONEIN-I (MT-I).//0.77:33:36//SCYLLA SERRATA (MUD CRAB).//P02805

F-PLACE1008627//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR)

(GIF) (GIFB).//0.14:44:31//HOMO SAPIENS (HUMAN).//P25713

F-PLACE1008629

F-PLACE1008630//PROTAMINE Z3 (SCYLLIORHININE Z3).//0.78:33:36//SCYLIORHINUS CANICULA (SPOTTED DOGFISH) (SPOTTED CATSHARK).//P30258

F-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN) (PLASMA KALLIKREIN SENSITIVE GLYCOPROTEIN 120) (PK-120).//1.7e-30:220:41//HOMO SAPIENS (HUMAN).//Q14624

F-PLACE1008650//PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1.//2.5e-10:106:31//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42384

F-PLACE1008693//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//1.0:36:38//MEDICAGO SCUTELLATA (SNAIL MEDIC).//P80321

F-PLACE1008696//NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-23KD) (CI-23KD) (TYKY SUBUNIT).//4.8e-14:47:80//HOMO SAPIENS (HUMAN).//000217

F-PLACE1008715//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION.//0.66:105:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38834

F-PLACE1008748//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.10:178:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-PLACE1008757//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3).//0.60:44:34//ESCHERICHIA COLI.//P33669

F-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2).//3.0e-69:191:80//MUS MUSCULUS (MOUSE).//035345

F-PLACE1008798//BACTERIOCIN LACTOBIN A.//1.0:34:41//LACTOBACILLUS AMYLOVORUS.//P80696

F-PLACE1008807//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.91:77:36//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1008808//REC1 PROTEIN.//0.45:39:30//USTILAGO MAYDIS (SMUT FUNGUS).//P14746

F-PLACE1008813

F-PLACE1008851//VERY HYPOTHETICAL 11.8 KD PROTEIN IN KTR3-DUR1,2 INTERGENIC REGION.//1.0:62:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P3830

9

F-PLACE1008854//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//1.0:82:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170

F-PLACE1008867//PATATIN T5 PRECURSOR (POTATO TUBER PROTEIN).//0.65:61:36 //SOLANUM TUBEROSUM (POTATO).//P15478

F-PLACE1008887//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-56:180:54//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-PLACE1008902

F-PLACE1008920

F-PLACE1008925//HYPOTHETICAL 41.2 KD PROTEIN IN GAPA-RND INTERGENIC REGION.//0.90:77:33//ESCHERICHIA COLI.//P76242

F-PLACE1008934//HYPOTHETICAL PROTEIN IN ADHS 5' REGION (ORF3) (FRAGMENT).//0.14:77:45//GLUCONOBACTER SUBOXYDANS.//005543

F-PLACE1008941//ZINC FINGER PROTEIN 141.//1.1e-17:45:95//HOMO SAPIENS (HUMAN).//Q15928

F-PLACE1008947//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B).//4.1e-14:136:39//MUS MUSCULUS (MOUSE).//P27790

F-PLACE1009020//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.74:37:48//BOS TAURUS (BOVINE).//P20072

F-PLACE1009027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.39:57:36//BALAENOPTERA MUSCULUS (BLUE WHALE).//P41301

F-PLACE1009039

F-PLACE1009045//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGION (F83).//0.48:32:43//ESCHERICHIA COLI.//P46879

F-PLACE1009048

F-PLACE1009050

F-PLACE1009060//HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III.

//4.9e-23:244:31//CAENORHABDITIS ELEGANS.//P34552

F-PLACE1009090//50S RIBOSOMAL PROTEIN L35.//1.0:27:51//MYCOPLASMA GENITALIUM.//P47439

F-PLACE1009091

F-PLACE1009094//NEL-LIKE PROTEIN (FRAGMENT).//3.6e-15:180:30//HOMO SAPIENS (HUMAN).//Q92832

F-PLACE1009099//ZINC FINGER PROTEIN 27 (ZFP-27) (MKR4 PROTEIN) (FRAGMENT).//1.4e-94:228:71//MUS MUSCULUS (MOUSE).//P10077

F-PLACE1009110//HIRUDIN HV1 (BUFRUDIN).//1.0:49:34//HIRUDINARIA MANILLESIS (BUFFALO LEECH).//P81492

F-PLACE1009111//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.4e-05:30:83//HOMO SAPIENS (HUMAN).//P39195

F-PLACE1009113//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.032:40:52//BOS TAURUS (BOVINE).//P20072

F-PLACE1009130//HYPOTHETICAL PROTEIN KIAA0032.//3.3e-37:214:38//HOMO SAPIENS (HUMAN).//Q15034

F-PLACE1009150//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.6e-32:56:76//HOMO SAPIENS (HUMAN).//P39195

F-PLACE1009155//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.2e-17:101:57//HOMO SAPIENS (HUMAN).//P39194

F-PLACE1009158//HYPOTHETICAL PROTEIN HKRFX (J1I).//0.0058:73:42//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P09711

F-PLACE1009166//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//0.0086:96:30//HOMO SAPIENS (HUMAN).//P49902

F-PLACE1009172//HYPOTHETICAL 8.7 KD PROTEIN IN GAPA-RND INTERGENIC REGION.//1.0:19:52//ESCHERICHIA COLI.//P76246

F-PLACE1009174//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.1e-17:47:82//HOMO SAPIENS (HUMAN).//P39194

F-PLACE1009183

F-PLACE1009186//HYPOTHETICAL 11.4 KD PROTEIN C13G6.04 IN CHROMOSOME I.//  
0.019:62:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09783

F-PLACE1009190//PALMITOYL-COA HYDROLASE (EC 3.1.2.2) (LONG-CHAIN FATTY-A  
CYL-COA HYDROLASE) (FRAGMENT).//0.027:53:28//RATTUS NORVEGICUS (RAT).//P  
80250

F-PLACE1009200//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//5.4e-28:84:71/  
/HOMO SAPIENS (HUMAN).//P39194

F-PLACE1009230//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.8e-12:50:74/  
/HOMO SAPIENS (HUMAN).//P39189

F-PLACE1009246//UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN  
(EC 1.10.2.2) (MITOCHONDRIAL HINGE PROTEIN) (CR7).//1.0:17:52//SOLANUM T  
UBEROSUM (POTATO).//P48504

F-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//6.6e  
-41:177:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34110

F-PLACE1009308//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).  
//0.00034:108:33//HOMO SAPIENS (HUMAN).//P26371

F-PLACE1009319//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95).//5.3e-16:84:50/  
/HOMO SAPIENS (HUMAN).//P78352

F-PLACE1009328//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.9e-82:263:67//H  
OMO SAPIENS (HUMAN).//P08547

F-PLACE1009335//60S RIBOSOMAL PROTEIN L32.//0.95:71:36//HOMO SAPIENS (HU  
MAN), MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT).//P02433

F-PLACE1009338//TRANSCRIPTION FACTOR HES-5 (HAIRY AND ENHANCER OF SPLIT  
5).//0.90:42:40//MUS MUSCULUS (MOUSE).//P70120

F-PLACE1009368//BASIC PROLINE-RICH PEPTIDE IB-1.//0.013:33:48//HOMO SAPI  
ENS (HUMAN).//P04281

F-PLACE1009375//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III.  
//0.0022:135:21//CAENORHABDITIS ELEGANS.//P34492

F-PLACE1009388//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//4.8e-22:73:65/  
/HOMO SAPIENS (HUMAN).//P39195

F-PLACE1009398//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.1e  
-83:223:65//HOMO SAPIENS (HUMAN).//P51523

F-PLACE1009404//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.  
//0.047:145:29//TRITICUM AESTIVUM (WHEAT).//P08489

F-PLACE1009410//TOXIN C13S1C1 PRECURSOR.//0.22:21:47//DENDROASPIS ANGUST  
ICEPS (EASTERN GREEN MAMBA).//P18329

F-PLACE1009434//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT K (EC 1.6.5.3) (F  
RAGMENT).//0.81:61:29//ANTHOCEROS FORMOSAE.//Q31791

F-PLACE1009443//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//9.  
1e-05:93:32//MUS MUSCULUS (MOUSE).//Q62203

F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-K  
INASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//6.4e-15:41:97//HOMO SAPIENS (HUM  
AN).//P42356

F-PLACE1009459//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I.  
//0.0011:119:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09874

F-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2e-34:10  
1:75//RATTUS NORVEGICUS (RAT).//P54319

F-PLACE1009476//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
.//0.086:21:52//HOMO SAPIENS (HUMAN).//P30808

F-PLACE1009477

F-PLACE1009493//HYPOTHETICAL 127.3 KD PROTEIN B0416.1 IN CHROMOSOME X.//  
1.4e-18:138:39//CAENORHABDITIS ELEGANS.//Q11069

F-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF E  
XCHANGE FACTOR).//9.4e-80:155:85//HOMO SAPIENS (HUMAN).//Q99418

F-PLACE1009539//GTP-BINDING NUCLEAR PROTEIN RAN/TC4.//1.0:76:26//GIARDIA  
LAMBLIA (GIARDIA INTESTINALIS).//P38543

F-PLACE1009542//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00016:31:77//

HOMO SAPIENS (HUMAN).//P39188

F-PLACE1009571//ATP SYNTHASE B CHAIN (EC 3.6.1.34) (SUBUNIT I).//0.88:11  
6:29//STREPTOCOCCUS PNEUMONIAE.//Q59952

F-PLACE1009581//50S RIBOSOMAL PROTEIN L32.//0.00023:37:51//RHODOBACTER C  
APSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P30788

F-PLACE1009595

F-PLACE1009596//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN  
C14B1.4 IN CHROMOSOME III.//2.1e-36:116:49//CAENORHABDITIS ELEGANS.//Q17  
963

F-PLACE1009607//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.8e-43:73:69//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE1009613

F-PLACE1009621//TRANSCRIPTION FACTOR BTF3 HOMOLOG 2.//0.91:29:44//HOMO S  
APIENS (HUMAN).//Q13891

F-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3e-22:132:47//DROSOP  
HILA MELANOGASTER (FRUIT FLY).//P25159

F-PLACE1009637//HYPOTHETICAL 18.1 KD PROTEIN IN CFXA 3' REGION.//0.30:28:  
57//BACTEROIDES VULGATUS.//P30905

F-PLACE1009639//LIPASE MODULATOR PRECURSOR (LIPASE HELPER PROTEIN).//0.2  
3:79:31//PSEUDOMONAS AERUGINOSA.//Q04591

F-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (BRAIN PROTEIN H19) (M  
H19) (FRAGMENT).//3.9e-126:227:96//MUS MUSCULUS (MOUSE).//P28660

F-PLACE1009665//IG KAPPA CHAIN V-I REGION (HAU).//0.52:89:35//HOMO SAPI  
ENS (HUMAN).//P01600

F-PLACE1009670//CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1  
.19) (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).//0.16:114:29//PAENIBAC  
ILLUS MACERANS (BACILLUS MACERANS).//P31835

F-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN  
C12G12.13C IN CHROMOSOME I.//9.6e-19:156:36//SCHIZOSACCHAROMYCES POMBE

(FISSION YEAST).//Q09876

F-PLACE1009721//MSF1 PROTEIN.//7.7e-23:176:33//SACCHAROMYCES CEREVIAE  
(BAKER'S YEAST).//P35200

F-PLACE1009731//AIG1 PROTEIN.//1.1e-09:91:43//ARABIDOPSIS THALIANA (MOUSE  
EAR CRESS).//P54120

F-PLACE1009763//HYPOTHETICAL 48.9 KD PROTEIN C24H6.12C IN CHROMOSOME I.//  
/8.3e-42:171:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09765

F-PLACE1009794//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.99:36:33//HOR  
DEUM VULGARE (BARLEY).//P17991

F-PLACE1009798//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT)  
.//2.6e-34:191:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09779

F-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//2.2e-19  
:190:33//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P38968

F-PLACE1009861//CATHEPSIN B PRECURSOR (EC 3.4.22.1).//4.4e-20:171:33//BO  
VINE TAURUS (BOVINE).//P07688

F-PLACE1009879//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC RE  
GION (ORF70).//0.99:30:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779

F-PLACE1009886

F-PLACE1009888//NONSTRUCTURAL POLYPROTEIN [CONTAINS: NONSTRUCTURAL PROTE  
IN NSP4] (FRAGMENT).//1.0:33:42//WESTERN EQUINE ENCEPHALITIS VIRUS.//P13  
896

F-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN C3F10.16C IN CHROMOSOME  
I.//3.1e-42:205:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10190

F-PLACE1009921

F-PLACE1009924//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.70:12  
8:29//TRYPANOSOMA BRUCEI BRUCEI.//P24499

F-PLACE1009925//ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.99  
:111:27//SACCHAROMYCES CEREVIAE (BAKER'S YEAST).//P30902

F-PLACE1009935//HYPOTHETICAL PROTEIN MJ0258.//0.063:75:32//METHANOCOCCUS

JANNASCHII.//Q57706

F-PLACE1009947//NEUROGRANIN (NG) (P17) (B-50 IMMUNOREACTIVE C-KINASE SUBSTRATE) (BICKS) (FRAGMENT).//0.33:51:45//BOS TAURUS (BOVINE).//P35722

F-PLACE1009971//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//0.022:84:27//MUS MUSCULUS (MOUSE).//P28575

F-PLACE1009992//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//0.00011:35:51//HOMO SAPIENS (HUMAN).//P13497

F-PLACE1009995//TROPOMYOSIN, SMOOTH MUSCLE/FIBROBLAST CTM1.//0.052:185:22//CIONA INTESTINALIS.//Q07068

F-PLACE1009997//TRANSCRIPTION ELONGATION FACTOR S-II (RNA POLYMERASE II ELONGATION FACTOR DMS-II) (TFIIS).//0.68:98:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//P20232

F-PLACE1010023//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//6.6e-06:111:32//CAENORHABDITIS ELEGANS.//Q18262

F-PLACE1010031//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//0.0024:72:33//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

F-PLACE1010053//HYPOTHETICAL PROTEIN HI0593.//0.83:24:45//HAEMOPHILUS INFLUENZAE.//P44022

F-PLACE1010069

F-PLACE1010074//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//0.00027:192:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331

F-PLACE1010076//HUNCHBACK PROTEIN (FRAGMENT).//0.80:39:30//SCIARA COPROPHILA (FUNGUS GNAT).//Q01790

F-PLACE1010083//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//2.7e-48:177:46//HOMO SAPIENS (HUMAN).//P98171

F-PLACE1010089//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 13) (DEUBIQUITINATING ENZYME 11) (KIAA0055).//7.9e-07:55:43//HOMO SAPIENS (H)

UMAN).//P40818

F-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.0e-107:232:90//RATTUS NORVEGICUS (RAT).//Q62671

F-PLACE1010102//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6).//1.0:33:45//METHANOCOCCUS JANNASCHII.//Q57649

F-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-47:200:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-PLACE1010106//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.2e-14:94:41//MUS MUSCULUS (MOUSE).//P11369

F-PLACE1010134//HYPOTHETICAL 171.5 KD HELICASE IN NUT1-ARO2 INTERGENIC REGION.//4.0e-28:78:76//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53115

F-PLACE1010148//GAR2 PROTEIN.//2.6e-05:180:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891

F-PLACE1010152//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//2.1e-59:227:54//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24574

F-PLACE1010181//MALE SPECIFIC SPERM PROTEIN MST87F.//0.39:12:58//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175

F-PLACE1010194//SPLICING FACTOR, ARGinine/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//1.4e-07:95:43//GALLUS GALLUS (CHICKEN).//P30352

F-PLACE1010202//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36).//0.094:109:29//RATTUS NORVEGICUS (RAT).//P47973

F-PLACE1010231//LANTIBIOTIC NISIN A PRECURSOR.//0.99:42:35//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P13068

F-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//6.0e-71:201:62//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25722

F-PLACE1010270

F-PLACE1010274//HYPOTHETICAL 16.2 KD PROTEIN C4F8.01 IN CHROMOSOME I.//4  
.4e-08:100:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//014177

F-PLACE1010293//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.9e-26:94:64//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE1010310//SYNAPSINS IA AND IB.//5.7e-09:89:37//RATTUS NORVEGICUS (RAT).//P09951

F-PLACE1010321//IMMEDIATE-EARLY PROTEIN IE180.//0.033:145:31//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-PLACE1010324//MAST CELL DEGRANULATING PEPTIDE (MCDP) (MCD).//0.60:25:48//MEGABOMBUS PENNSYLVANICUS (AMERICAN COMMON BUMBLEBEE).//P04567

F-PLACE1010329//TOXIN S5C10.//1.0:39:33//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).//P01419

F-PLACE1010341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//0.0049:49:55//  
HOMO SAPIENS (HUMAN).//P39189

F-PLACE1010362//VARIANT-SURFACE-GLYCOPROTEIN PHOSPHOLIPASE C (EC 3.1.4.47) (VSG LIPASE) (GLYCOSYLPHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (GPI-PLC).//0.0034:89:30//TRYPANOSOMA CRUZI.//015886

F-PLACE1010364//NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B17) (CI-B17).//1.0:40:35//SUS SCROFA (PIG).//Q29259

F-PLACE1010383

F-PLACE1010401//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//0.10:174:22//  
/RATTUS NORVEGICUS (RAT).//P41777

F-PLACE1010481//HYPOTHETICAL 71.9 KD PROTEIN B0285.5 IN CHROMOSOME III.//1.5e-21:170:35//CAENORHABDITIS ELEGANS.//P46555

F-PLACE1010491//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//1.0:31:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490

F-PLACE1010492//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I.

//0.77:97:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09874  
F-PLACE1010522//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.7  
4:45:37//HOMO SAPIENS (HUMAN).//P22531  
F-PLACE1010529//DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)].//0.70:58:39//VIGNA ACONITIFOLIA (MOTHBEAN).//P32296  
F-PLACE1010547//HYPOTHETICAL 31.0 KD PROTEIN IN BUD9-RME1 INTERGENIC REGION.//0.17:68:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53227  
F-PLACE1010562//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.50:48:29//PORPHYRA PURPUREA.//P51255  
F-PLACE1010579//HYPOTHETICAL PROTEIN HI1571.//0.29:37:43//HAEMOPHILUS INFLUENZAE.//P44260  
F-PLACE1010580//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//3.3e-38:1  
78:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747  
F-PLACE1010599//PEROXISOMAL MEMBRANE PROTEIN PER10 (PEROXIN-14).//4.6e-1  
7:192:31//PICHIA ANGUSTA (YEAST) (HANSENULA POLYMORPHA).//P78723  
F-PLACE1010616//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3' REGION.//0.44:32:3  
7//PSEUDOMONAS PUTIDA.//P25753  
F-PLACE1010622//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//5.0e-06:102:  
42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323  
F-PLACE1010624//SALIVARY PROLINE-RICH PROTEIN PO (ALLEL K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00036:134:32//HOMO SAPIENS (HUMAN).//P10162  
F-PLACE1010628  
F-PLACE1010629//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.7e-12:37:81//  
/HOMO SAPIENS (HUMAN).//P39194  
F-PLACE1010630  
F-PLACE1010631//WNT-5B PROTEIN (FRAGMENT).//0.49:62:30//EUMECES SKILTONI

ANUS (WESTERN SKINK).//P28118

F-PLACE1010661//MATERNAL EXUPERANTIA 2 PROTEIN.//1.0:95:30//DROSOPHILA P  
SEUDOBOBSCURA (FRUIT FLY).//Q24617

F-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//3.2e-05:117:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332

F-PLACE1010702//ZINC FINGER PROTEIN 195.//1.4e-62:117:62//HOMO SAPIENS (HUMAN).//014628

F-PLACE1010714

F-PLACE1010720//CHROMOSOME ASSEMBLY PROTEIN XCAP-C.//1.1e-64:176:76//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50532

F-PLACE1010739//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.97:31:41//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612

F-PLACE1010743//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//3.8e-05:253:30//MUS MUSCULUS (MOUSE).//P05143

F-PLACE1010761//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//1.5e-14:175:25//CAENORHABDITIS ELEGANS.//Q09217

F-PLACE1010771//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//1.3e-120:216:8//MUS MUSCULUS (MOUSE).//Q02614

F-PLACE1010786//CENTROSOMIN (ARROW PROTEIN).//0.97:133:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54623

F-PLACE1010800//HYPOTHETICAL 31.7 KD PROTEIN IN TRAX-FINO INTERGENIC REGION (ORFC).//0.0060:111:31//ESCHERICHIA COLI.//Q99390

F-PLACE1010802//UREASE ACCESSORY PROTEIN UREI.//0.82:44:29//BACILLUS SP. (STRAIN TB-90).//Q07415

F-PLACE1010811//CYTOCHROME C-551 (C551).//0.99:42:38//ECTOTHIORHODOSPIRA HALOCHLORIS.//P38587

F-PLACE1010833//CALTRACTIN, ISOFORM 1 (CENTRIN).//2.8e-09:90:34//HOMO SA

PIENS (HUMAN).//P41208

F-PLACE1010856//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMBARUS C LARKII (RED SWAMP CRAYFISH).//P55848

F-PLACE1010857//IG ALPHA-1 CHAIN C REGION.//0.49:73:34//GORILLA GORILLA GORILLA (LOWLAND GORILLA).//P20758

F-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.2e-56:173:58//HOMO SAPIENS (HUMAN).//Q05481

F-PLACE1010877//HEAT SHOCK PROTEIN 82.//0.13:130:25//ZEA MAYS (MAIZE).//Q08277

F-PLACE1010891//HYPOTHETICAL 8.2 KD PROTEIN IN BLTR-SPOIIIC INTERGENIC REGION.//0.95:51:27//BACILLUS SUBTILIS.//P54436

F-PLACE1010896//SERINE/THREONINE-PROTEIN KINASE PTK1/STK1 (EC 2.7.1.-).//0.98:71:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36002

F-PLACE1010900//HYPOTHETICAL PROTEIN HI0840.//1.0:42:30//HAEMOPHILUS INF LUENZAE.//P44897

F-PLACE1010916//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB3.//0.060:59:35 //OVIS ARIES (SHEEP).//P02444

F-PLACE1010917//E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN).//0.71:141:24//BOVINE CORONAVIRUS (STRAIN L9).//P25191

F-PLACE1010925//HYPOTHETICAL 8.1 KD PROTEIN.//1.0:17:58//THERMOPROTEUS T ENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19285

F-PLACE1010926//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269.//0.011:51:45 //HOMO SAPIENS (HUMAN).//Q92558

F-PLACE1010942//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15).//3.1e-09:64:37//MUS MUSCULUS (MOUSE).//P42567

F-PLACE1010944//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//0.17 :71:38//BOS TAURUS (BOVINE).//P41987

F-PLACE1010947

F-PLACE1010954//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//0.011:144:26/

/HOMO SAPIENS (HUMAN).//P09493

F-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//1.1e-60:136:52//DROSOPHILA MELA  
NOGASTER (FRUIT FLY).//P45890

F-PLACE1010965

F-PLACE1011026//PERIOD CLOCK PROTEIN (FRAGMENT).//1.0:64:31//DROSOPHILA  
ANANASSAE (FRUIT FLY).//Q03293

F-PLACE1011032//RIBONUCLEASE HI (EC 3.1.26.4) (RNASE HI) (RIBONUCLEASE H  
) (RNASE H).//1.0:32:37//SALMONELLA TYPHIMURIUM.//P23329

F-PLACE1011041//HOMEobox PROTEIN VAB-7.//0.36:65:30//CAENORHABDITIS ELEG  
ANS.//Q93899

F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERAS  
E BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PL  
C-154).//1.3e-22:58:93//RATTUS NORVEGICUS (RAT).//P10687

F-PLACE1011054//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.6e-07:38:73/  
/HOMO SAPIENS (HUMAN).//P39195

F-PLACE1011056//HISTONE H1.//2.2e-10:109:41//PISUM SATIVUM (GARDEN PEA).  
//P08283

F-PLACE1011057

F-PLACE1011090//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FL05 INTERGENIC REG  
ION.//1.8e-07:133:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38892

F-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//5  
.4e-25:63:88//RATTUS NORVEGICUS (RAT).//Q07803

F-PLACE1011114//PUTATIVE ATP-DEPENDENT RNA HELICASE C1F7.02C.//8.4e-31:1  
57:45//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09916

F-PLACE1011133//SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (9.5S ALPHA-1-  
GLYCOPROTEIN).//0.92:58:31//HOMO SAPIENS (HUMAN).//P02743

F-PLACE1011143//PROBABLE E5 PROTEIN.//0.24:42:35//HUMAN PAPILLOMAVIRUS T  
YPE 31.//P17385

F-PLACE1011160//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.

88:98:27//GLYCINE MAX (SOYBEAN).//Q02917

F-PLACE1011165//HISTIDINE-RICH PROTEIN.//0.013:13:76//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGRAL).//P14586

F-PLACE1011185//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.4e-13:98:50//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1011203

F-PLACE1011214//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:48:27//EQUUS ASINUS (DONKEY).//P92479

F-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.---).//1.9e-15:162:31//S TREPTOMYCES ANTIBIOTICUS.//Q03326

F-PLACE1011221//ANTITHROMBIN-III HOMOLOG.//0.84:74:33//FOWLPOX VIRUS (ISOLATE HP-438 [MUNICH]).//P14369

F-PLACE1011229//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//3.5e-86:218:68//HOMO SAPIENS (HUMAN).//Q13107

F-PLACE1011263//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//3.0e-07:99:36//HOMO SAPIENS (HUMAN).//Q01485

F-PLACE1011273

F-PLACE1011291//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).//0.011:36:50//RATTUS NORVEGICUS (RAT).//P20468

F-PLACE1011296//HOMEobox PROTEIN DLX-6.//0.76:55:32//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q98877

F-PLACE1011310//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-BINDING PROTEIN).//0.46:43:44//PETUNIA SP. (PETUNIA).//Q07060

F-PLACE1011325//HYPOTHETICAL 222.8 KD PROTEIN C1F3.06C IN CHROMOSOME I.//0.00021:171:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10411

F-PLACE1011332//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR.//7.3e-27:113:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q05211

F-PLACE1011340//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.6e-07:40:62//

HOMO SAPIENS (HUMAN).//P39188

F-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//2.2e-54:227:44//MUS MUSCULUS (MOUSE).//Q61703

F-PLACE1011375//PROBABLE E5 PROTEIN.//0.93:28:57//HUMAN PAPILLOMAVIRUS T YPE 51.//P26553

F-PLACE1011399//HISTONE H2B-IV.//0.19:129:27//VOLVOX CARTERI.//P16868

F-PLACE1011419

F-PLACE1011433//ZINC FINGER PROTEIN GLI3 (FRAGMENT).//3.4e-05:133:24//GALLUS GALLUS (CHICKEN).//P55879

F-PLACE1011452//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.9e-25:76:63//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1011465//ECTODERMAL DYSPLASIA PROTEIN (EDA PROTEIN).//0.97:36:41//HOMO SAPIENS (HUMAN).//Q92838

F-PLACE1011472//METALLOTHIONEIN-1 (CUMT-1).//0.084:55:30//HOMARUS AMERICANUS (AMERICAN LOBSTER).//P29499

F-PLACE1011477//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1).//0.028:129:34//CLOSTRIDIUM THERMOCELLUM.//Q06852

F-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//2.9e-13:147:31//BRASSICA OLERACEA (CAULIFLOWER).//P52178

F-PLACE1011503//PUTATIVE FERREDOXIN-LIKE PROTEIN IN PURL-DPJ INTERGENIC REGION (086).//0.66:32:40//ESCHERICHIA COLI.//P52102

F-PLACE1011520

F-PLACE1011563//LORICRIN.//0.00023:112:39//HOMO SAPIENS (HUMAN).//P23490

F-PLACE1011567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//9.2e-31:78:76//HOMO SAPIENS (HUMAN).//P39195

F-PLACE1011576//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.5e-32:45:86//HOMO SAPIENS (HUMAN).//Q05481

F-PLACE1011586//N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (OMEGA-CONOTOXIN  
-SENSITIVE N- TYPE, BRAIN CALCIUM CHANNEL ALPHA-1 SUBUNIT).//0.26:81:37/  
/HOMO SAPIENS (HUMAN).//Q00975

F-PLACE1011635//IMMEDIATE-EARLY PROTEIN IE180.//0.00045:170:30//PSEUDORA  
BIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-PLACE1011641

F-PLACE1011643//CUTICLE COLLAGEN 40.//1.0:128:32//CAENORHABDITIS ELEGANS  
.//P34804

F-PLACE1011646//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.1e-15:44:63//  
● HOMO SAPIENS (HUMAN).//P39188

F-PLACE1011649//HYPOTHETICAL PROTEIN F-215.//0.48:106:34//HUMAN ADENOVIR  
US TYPE 2.//P03291

F-PLACE1011650

F-PLACE1011664//CROOKED NECK PROTEIN.//1.2e-79:201:68//DROSOPHILA MELANO  
GASTER (FRUIT FLY).//P17886

F-PLACE1011675//FERREDOXIN.//1.0:44:29//METHANOCOCCUS THERMOLITHOTROPHIC  
US.//P21305

F-PLACE1011682//HYPOTHETICAL 7.0 KD PROTEIN IN RPS26A-COX4 INTERGENIC RE  
GION.//1.0:40:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53098

● F-PLACE1011719//NEUROTOXIN TX2-6.//0.90:31:35//PHONEUTRIA NIGRIVENTER (B  
RAZILIAN ARMED SPIDER).//P29425

F-PLACE1011725//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDI  
NG PROTEIN).//0.0065:125:25//RATTUS NORVEGICUS (RAT).//Q63083

F-PLACE1011729//SRY-RELATED PROTEIN LG27 (FRAGMENT).//0.97:48:39//EUBLEP  
HARIS MACULARIUS.//P40654

F-PLACE1011749

F-PLACE1011762//D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN).  
//0.028:91:39//MUS MUSCULUS (MOUSE).//Q60925

F-PLACE1011778

F-PLACE1011783//EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1).//0.97:48:43//MUS MUSCULUS (MOUSE).//P20863

F-PLACE1011858//COLLAGEN 1(X) CHAIN PRECURSOR.//0.0027:154:33//BOS TAURUS (BOVINE).//P23206

F-PLACE1011874//BACTERIOCHLOROPHYLL A PROTEIN (BCHL A PROTEIN) (BCP).//1.0:60:26//PROSTHECOCHLORIS AESTUARI.//P11741

F-PLACE1011875//HYPOTHETICAL 6.6 KD PROTEIN IN GP54-ALT INTERGENIC REGION.//0.99:34:35//BACTERIOPHAGE T4.//P39495

F-PLACE1011891//SMOOTHELIN.//0.018:122:31//HOMO SAPIENS (HUMAN).//P53814

F-PLACE1011896//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//6.3e-09:203:35//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-PLACE1011922//CRYPTDIN-RELATED PROTEIN 4C-2 PRECURSOR (CRS4C).//0.067:37:48//MUS MUSCULUS (MOUSE).//P50715

F-PLACE1011923//SERINE/THREONINE-PROTEIN KINASE SNK (EC 2.7.1.-) (SERUM INDUCIBLE KINASE).//1.5e-83:175:89//MUS MUSCULUS (MOUSE).//P53351

F-PLACE1011962//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR.//0.50:46:41//SCHIZOPHYLLUM COMMUNE (BRACKET FUNGUS).//Q02593

F-PLACE1011964//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.6e-05:47:51//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-PLACE1011982//APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).//0.98:83:31//PLASMODIUM FRAGILE.//P22622

F-PLACE1011995

F-PLACE1012031//HYPOTHETICAL PROTEIN KIAA0254.//0.032:62:33//HOMO SAPIENS (HUMAN).//Q92543

F-PLACE2000003//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//5.4e-18:63:73//HOMO SAPIENS (HUMAN).//P39193

F-PLACE2000006//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.14:20:50//BOS TAURUS (BOVINE).//P20072

F-PLACE2000007//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0045:176:30//MU

S MUSCULUS (MOUSE).//P05143

F-PLACE2000011//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.6e-25:57:78/  
/HOMO SAPIENS (HUMAN).//P39194

F-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.0001  
3:237:27//CAENORHABDITIS ELEGANS.//Q09475

F-PLACE2000015//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.4e-33:60:80/  
/HOMO SAPIENS (HUMAN).//P39193

F-PLACE2000017//FOLATE RECEPTOR BETA PRECURSOR (FR-BETA) (FOLATE RECEPTO  
R 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEI  
N) (FBP).//1.0:83:31//HOMO SAPIENS (HUMAN).//P14207

F-PLACE2000021//EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROS  
INE-PROTEIN KINASE RECEPTOR CEK8).//0.99:103:26//GALLUS GALLUS (CHICKEN)  
.//Q07496

F-PLACE2000030//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.69:29:44//DROSOP  
HILA MELANOGASTER (FRUIT FLY).//Q01642

F-PLACE2000033//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//1.1e-05:74:41//ST  
REPTOMYCES ANTIBIOTICUS.//Q03326

F-PLACE2000034//AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIEN  
T AXONAL GLYCOPROTEIN 1).//6.7e-18:191:35//HOMO SAPIENS (HUMAN).//Q02246

F-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C).//4.7e-80:  
163:96//RATTUS NORVEGICUS (RAT).//P38650

F-PLACE2000047//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//6.4e-06:63:49  
//HOMO SAPIENS (HUMAN).//P39191

F-PLACE2000050//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.2e-22:74:64/  
/HOMO SAPIENS (HUMAN).//P39192

F-PLACE2000061

F-PLACE2000062//GLUCOSE STARVATION-INDUCIBLE PROTEIN B (GENERAL STRESS P  
ROTEIN B).//1.9e-06:108:37//BACILLUS SUBTILIS.//P26907

F-PLACE2000072//ZINC FINGER PROTEIN 165.//3.5e-34:175:49//HOMO SAPIENS (

HUMAN).//P49910

F-PLACE2000097//RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A).//0.36:39:38//ONDATRA ZIBETHICUS (MUSKRAT).//P00681

F-PLACE2000100

F-PLACE2000103//TUBULIN ALPHA-4 CHAIN (FRAGMENTS).//0.18:32:37//ZEA MAYS (MAIZE).//P33626

F-PLACE2000111//CMRF35 ANTIGEN PRECURSOR.//0.056:107:27//HOMO SAPIENS (HUMAN).//Q08708

F-PLACE2000115//DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7) (DAP EPIMERASE) (FRAGMENT).//1.0:21:52//CLOSTRIDIUM PERFRINGENS.//Q46185

F-PLACE2000124//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.4e-37:108:68//HOMO SAPIENS (HUMAN).//P39194

F-PLACE2000132//PROBABLE MEMBRANE ANTIGEN GP85.//0.99:133:29//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03224

F-PLACE2000136//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR (VIP-R-2) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR) (PACAP TYPE III RECEPTOR) (PACAP-R-3).//0.83:65:32//MUS MUSCULUS (MOUSE).//P41588

F-PLACE2000140

F-PLACE2000164//TIPD PROTEIN.//5.7e-12:190:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//015736

F-PLACE2000170//BACTERIOCIN CARNOBACTERIOCIN BM1 PRECURSOR (CARNOBACTERIOCIN B1).//1.0:30:26//CARNOBACTERIUM PISCICOLA.//P38579

F-PLACE2000172

F-PLACE2000176//HYPOTHETICAL PROTEIN AF0526.//0.76:44:43//ARCHAEOGLOBUS FULGIDUS.//029724

F-PLACE2000187//EM-LIKE PROTEIN GEA6.//0.84:42:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q02973

F-PLACE2000216

F-PLACE2000223//NEUROTOXIN III (LQQ III).//0.99:38:34//LEIURUS QUINQUESTRIATUS QUINQUESTRIATUS (EGYPTIAN SCORPION).//P01487

F-PLACE2000235

F-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).//5.1e-37:121:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-PLACE2000264//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//2.4e-05:77:42//HOMO SAPIENS (HUMAN).//P39191

F-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//5.3e-46:232:45//TRIPNEUSTES GRATILLA (HAWAIIAN SEA URCHIN).//P23098

F-PLACE2000302//TRICHOHYALIN.//1.5e-06:215:29//ORYCTOLAGUS CUNICULUS (RABBIT).//P37709

F-PLACE2000305//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.3e-06:33:66//HOMO SAPIENS (HUMAN).//P39188

F-PLACE2000317//TOXIN C13S1C1 PRECURSOR.//0.44:45:33//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329

F-PLACE2000335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//7.9e-08:35:71//HOMO SAPIENS (HUMAN).//P39195

F-PLACE2000341//SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+))/GLUCOSE COTRANSPORTER 1 (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).//0.014:141:24//ORYCTOLAGUS CUNICULUS (RABBIT).//P11170

F-PLACE2000342//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//5.7e-09:96:38//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

F-PLACE2000347//ZINC FINGER PROTEIN 177.//5.9e-05:49:53//HOMO SAPIENS (HUMAN).//Q13360

F-PLACE2000359//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.5e-10:69:52//HOMO SAPIENS (HUMAN).//P39194

F-PLACE2000366

F-PLACE2000371//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN

.)//1.5e-05:216:29//HOMO SAPIENS (HUMAN).//P54259  
F-PLACE2000373//MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT).//0.27:63:33//HOMO SAPIENS (HUMAN).//Q99583  
F-PLACE2000379//HYPOTHETICAL GENE 1 PROTEIN.//0.72:120:31//EQUINE HERPES VIRUS TYPE 1 (STRAIN AB4P) (EHV-1).//P28978  
F-PLACE2000394//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.95:40:42//HOMO SAPIENS (HUMAN).//P02811  
F-PLACE2000398//RIBONUCLEASE PRECURSOR (EC 3.1.27.-).//0.88:88:31//AEROMONAS HYDROPHILA.//Q07465  
● F-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//7.6e-16:180:39//HOMO SAPIENS (HUMAN).//P14209  
F-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--T RNA LIGASE) (LEURS).//1.7e-94:243:64//CAENORHABDITIS ELEGANS.//Q09996  
F-PLACE2000411//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//1.2e-09:78:39//MUS MUSCULUS (MOUSE).//Q60676  
F-PLACE2000419//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.6e-20:61:62//HOMO SAPIENS (HUMAN).//P39188  
● F-PLACE2000425//HYPOTHETICAL 11.9 KD PROTEIN IN MSB2-UGA1 INTERGENIC REGION.//0.98:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53211  
F-PLACE2000427//INSULIN PRECURSOR.//0.98:55:34//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P30407  
F-PLACE2000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//7.5e-07:65:50//HOMO SAPIENS (HUMAN).//P39188  
F-PLACE2000435  
F-PLACE2000438//HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III.//4.7e-66:178:47//CAENORHABDITIS ELEGANS.//P34678  
F-PLACE2000450//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.1e-23:88:62//

/HOMO SAPIENS (HUMAN).//P39195

F-PLACE2000455//TOXIN II (TOXIN II.10.9.2) (FRAGMENT).//0.093:18:44//CEN

TRUROIDES LIMPIDUS LIMPIDUS (MEXICAN SCORPION).//P45630

F-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.1e-23:165:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P33450

F-PLACE2000465//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.6e-23:73:63//

HOMO SAPIENS (HUMAN).//P39188

F-PLACE2000477//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.4e-37:90:78//

HOMO SAPIENS (HUMAN).//P39194

F-PLACE3000004//EYES ABSENT HOMOLOG 3.//1.1e-09:27:100//MUS MUSCULUS (MOUSE).//P97480

F-PLACE3000009//PUTATIVE CUTICLE COLLAGEN C09G5.6.//0.0061:148:34//CAENORHABDITIS ELEGANS.//Q09457

F-PLACE3000020//ADENYLYATE CYCLASE, OLFACTIVE TYPE (EC 4.6.1.1) (TYPE III) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//8.8e-93:193:92//RATTUS NORVEGICUS (RAT).//P21932

F-PLACE3000029//50S RIBOSOMAL PROTEIN L31E.//0.15:50:38//METHANOCOCCUS JANNASCHII.//P54009

F-PLACE3000059//TCP1-CHAPERONIN COFACTOR A.//0.96:50:34//BOS TAURUS (BOVINE).//P48427

F-PLACE3000070//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3' REGION.//0.29:22:59//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898

F-PLACE3000103//LYSIS PROTEIN (E PROTEIN) (GPE).//0.99:53:32//BACTERIOPHAGE ALPHA-3.//P31280

F-PLACE3000119//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//5.4e-41:87:78//HOMO SAPIENS (HUMAN).//P39189

F-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC15.//1.0e-07:269:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P22224

F-PLACE3000124//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.2e-29:97:73//

HOMO SAPIENS (HUMAN).//P39188

F-PLACE3000136//PARS INTERCEREBRALIS MAJOR PEPTIDE D1 (PMP-D1).//0.77:26  
:42//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//P80059

F-PLACE3000142//HYPOTHETICAL 7.1 KD PROTEIN IN NAD2 3' REGION (ORF 63).//  
0.82:34:41//MARCHANTIA POLYMORPHA (LIVERWORT).//P38468

F-PLACE3000145//TENSIN.//3.5e-91:238:74//GALLUS GALLUS (CHICKEN).//Q0420  
5

F-PLACE3000147//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.4e-30:61:65/  
/HOMO SAPIENS (HUMAN).//P39194

F-PLACE3000148//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVER  
SE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.4e-18:226:34//GIBBON A  
PE LEUKEMIA VIRUS.//P21414

F-PLACE3000155//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.00014  
:107:33//ZEA MAYS (MAIZE).//P14918

F-PLACE3000156//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVER  
SE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//2.7e-19:169:30//BABOON E  
NDOGENOUS VIRUS (STRAIN M7).//P10272

F-PLACE3000157//PROBABLE SERINE/THREONINE-PROTEIN KINASE CY50.16 (EC 2.7  
.1.-).//0.0061:92:30//MYCOBACTERIUM TUBERCULOSIS.//Q11053

F-PLACE3000158//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//5.7e-49:56:80/  
/HOMO SAPIENS (HUMAN).//P39189

F-PLACE3000160//DNA TRANSFORMATION PROTEIN TFOX (COMPETENCE ACTIVATOR) (  
PROTEIN SXY).//0.39:94:34//HAEMOPHILUS INFLUENZAE.//P43779

F-PLACE3000169//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//5.6e-28:99:59/  
/HOMO SAPIENS (HUMAN).//P39193

F-PLACE3000194//PROLINE-RICH PROTEIN LAS17.//0.91:80:36//SACCHAROMYCES C  
EREVISIAE (BAKER'S YEAST).//Q12446

F-PLACE3000197//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PR  
OTEIN) (NF-M).//0.24:119:32//GALLUS GALLUS (CHICKEN).//P16053

F-PLACE3000199//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.76:87:37//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-PLACE3000207//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.5e-09:32:78//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE3000208

F-PLACE3000218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.2e-34:96:70//  
/HOMO SAPIENS (HUMAN).//P39194

F-PLACE3000220//OSTEOCALCIN (GAMMA-CARBOXYGLUTAMIC ACID-CONTAINING PROTEIN) (BONE GLA- PROTEIN) (BGP).//0.46:13:53//CANIS FAMILIARIS (DOG).//P81  
455

F-PLACE3000221//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.8e-24:178:45//  
/HOMO SAPIENS (HUMAN).//P39188

F-PLACE3000226//30S RIBOSOMAL PROTEIN S18.//0.98:38:34//NEISSERIA GONORRHOEAE.//007815

F-PLACE3000230//METALLOTHIONEIN (MT).//0.97:25:48//OREOCHROMIS MOSSAMBIUS (MOZAMBIQUE TILAPIA) (TILAPIA MOSSAMBICA).//P52726

F-PLACE3000242//MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN).//8.0e-21  
:121:39//HOMO SAPIENS (HUMAN).//P43361

F-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//2.3e-125  
:264:87//MUS MUSCULUS (MOUSE).//P53995

F-PLACE3000254//RTOA PROTEIN (RATIO-A).//0.99:142:23//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54681

F-PLACE3000271//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.2e-12:63:53//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE3000276//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//1.0:55:38//HOMO SAPIENS (HUMAN).//P27658

F-PLACE3000304//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
.//0.0028:31:54//HOMO SAPIENS (HUMAN).//P30808

F-PLACE3000310//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN

).//0.98:82:34//RATTUS NORVEGICUS (RAT).//P54258  
F-PLACE3000320  
F-PLACE3000322//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR.//  
2.2e-22:61:52//ORYZA SATIVA (RICE).//P25074  
F-PLACE3000331//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.  
32:15:53//HOMO SAPIENS (HUMAN).//P22532  
F-PLACE3000339//CHORION PROTEIN S19.//0.34:89:37//DROSOPHILA VIRILIS (FR  
UIT FLY).//P24516  
F-PLACE3000341//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRA  
GMENT).//1.0:47:38//COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P24968  
F-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULU (EC 2.7.1.-).//3.9e  
-50:168:60//CAENORHABDITIS ELEGANS.//P46549.  
F-PLACE3000352//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.8e-29:76:71/  
/HOMO SAPIENS (HUMAN).//P39194  
F-PLACE3000353//POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.  
41) (PROTEIN- UDP ACETYLGLACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTI  
DE, N- ACETYLGLACTOSAMINYLTRANSFERASE) (GALNAC-T1).//3.0e-09:100:41//HO  
MO SAPIENS (HUMAN).//Q10472  
F-PLACE3000362//HYPOTHETICAL PROTEIN TP0064.//1.0:75:26//TREPONEMA PALLI  
DUM.//083103  
F-PLACE3000363//METALLOTHIONEIN (MT).//0.067:42:33//ASTACUS FLUVIATILIS  
(BROAD-FINGERED CRAYFISH) (ASTACUS ASTACUS).//P55951  
F-PLACE3000365//LYSIS PROTEIN (E PROTEIN) (GPE).//1.0:65:27//BACTERIOPHA  
GE PHI-K.//Q38040  
F-PLACE3000373//RETROVIRUS-RELATED ENV POLYPYPROTEIN.//1.5e-18:90:47//HOMO  
SAPIENS (HUMAN).//P10267  
F-PLACE3000388  
F-PLACE3000399//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//6.3e-45:60:75/  
/HOMO SAPIENS (HUMAN).//P39193

F-PLACE3000400

F-PLACE3000401//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.6e-09:46:73//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE3000402//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.036:43:44//HO  
MO SAPIENS (HUMAN).//P39188

F-PLACE3000405//POSTERIOR PITUITARY PEPTIDE.//0.70:25:40//BOS TAURUS (BO  
VINE).//P01154

F-PLACE3000406//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//4.3e-09:49:67//  
/HOMO SAPIENS (HUMAN).//P39195

● F-PLACE3000413//MALE SPECIFIC SPERM PROTEIN MST87F.//0.12:42:40//DROSOPH  
ILA MELANOGASTER (FRUIT FLY).//P08175

F-PLACE3000416//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.67:236:21//B  
OS TAURUS (BOVINE).//P35662

F-PLACE3000425//PROLINE-RICH PEPTIDE P-B.//0.45:19:42//HOMO SAPIENS (HUM  
AN).//P02814

F-PLACE3000455//AMELOGENIN, CLASS I PRECURSOR.//0.0073:81:43//BOS TAURUS  
(BOVINE).//P02817

F-PLACE3000475//8.6 KD TRANSGlutaminase SUBSTRATE.//1.0:53:32//TACHYPLEU  
S TRIDENTATUS (JAPANESE HORSESHOE CRAB).//P81281

● F-PLACE3000477//MUSCARINIC TOXIN 7 (MT-7).//0.13:55:32//DENDROASPIS ANGU  
STICEPS (EASTERN GREEN MAMBA).//P80970

F-PLACE4000009//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGM  
ENT).//7.0e-19:180:27//HOMO SAPIENS (HUMAN).//P35749

F-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//  
3.2e-15:193:30//HOMO SAPIENS (HUMAN).//P46100

F-PLACE4000034//BRIDE OF SEVENLESS PROTEIN PRECURSOR.//0.0024:97:29//DRO  
SOPHILA MELANOGASTER (FRUIT FLY).//P22815

F-PLACE4000049//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.8e-32:79:75//  
/HOMO SAPIENS (HUMAN).//P39194

F-PLACE4000052//ATP-BINDING CASSETTE TRANSPORTER 1.//2.2e-99:178:97//MUS  
MUSCULUS (MOUSE).//P41233

F-PLACE4000063//IMMEDIATE-EARLY PROTEIN.//0.0017:159:25//HERPESVIRUS SAI  
MIRI (STRAIN 11).//Q01042

F-PLACE4000089

F-PLACE4000093

F-PLACE4000100//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.5e-14:68:60//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE4000106//1A PROTEIN [CONTAINS: HELICASE; METHYLTRANSFERASE] .//1.0  
:46:41//BROAD BEAN MOTTLE VIRUS.//Q00020

F-PLACE4000128//HYPOTHETICAL PROTEIN E-115.//0.00020:101:30//HUMAN ADENO  
VIRUS TYPE 2.//P03290

F-PLACE4000129//CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.  
9 KD PANCRONULIN).//0.15:57:31//HOMO SAPIENS (HUMAN).//P22528

F-PLACE4000131

F-PLACE4000147//COMPETENCE PHEROMONE PRECURSOR.//1.0:45:24//BACILLUS SUB  
TILIS.//P45453

F-PLACE4000156//ZINC FINGER PROTEIN 136.//2.1e-88:194:59//HOMO SAPIENS (HUMAN).//P52737

F-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//0.083:148:  
26//HOMO SAPIENS (HUMAN).//P52746

F-PLACE4000211//CALPHOTIN.//0.20:43:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q02910

F-PLACE4000222//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.1e-05:20:85//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE4000230//DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) / THYMIDYLATE SYNTHASE (EC 2.1.1.45) (DHFR-TS).//1.0:96:28//TRYPANOSOMA BRUCEI BRUCEI.//Q27

783

F-PLACE4000233

F-PLACE4000247//METALLOTHIONEIN (MT).//1.0e-05:34:41//PLEURONECTES PLATE  
SSA (PLAICE).//P07216

F-PLACE4000250//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN).//0.99:33:42//  
CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (CAEV).//P31834

F-PLACE4000252//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.42:24:45//DROSOP  
HILA MELANOGASTER (FRUIT FLY).//Q01643

F-PLACE4000259//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-).//3.5e-09:1  
89:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32639

F-PLACE4000261//PEREGRIN (BR140 PROTEIN).//5.0e-11:103:37//HOMO SAPIENS  
(HUMAN).//P55201

F-PLACE4000269//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//0.037:181  
:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386

F-PLACE4000270//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).//1.0:46  
:39//MUS MUSCULUS (MOUSE).//P70375

F-PLACE4000300//50S RIBOSOMAL PROTEIN L32.//0.81:28:46//THERMUS AQUATICU  
S (SUBSP. THERMOPHILUS).//P80339

F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARG  
ET PROTEIN).//1.6e-29:44:93//HOMO SAPIENS (HUMAN).//P42345

F-PLACE4000323

F-PLACE4000326//PARATHYMOSEN.//0.0018:54:48//HOMO SAPIENS (HUMAN).//P209  
62

F-PLACE4000344//EPIDERMAL GROWTH FACTOR (EGF) (FRAGMENT).//0.97:28:42//S  
US SCROFA (PIG).//Q00968

F-PLACE4000367//NEUROTOXIN 1 (TOXIN SHP-I) (SHNA) (NEUROTOXIN SHI).//1.0  
:33:36//STOICHACTIS HELIANTHUS (CARIBBEAN SEA ANEMONE) (STICHODACTYLA HE  
LIANTHUS).//P19651

F-PLACE4000369//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.071:4  
2:42//SORGHUM VULGARE (SORGHUM).//P24152

F-PLACE4000379//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.4e-16:54:77/

/HOMO SAPIENS (HUMAN).//P39193

F-PLACE4000387//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//

0.25:21:52//HORDEUM VULGARE (BARLEY), AND SECALE CEREALE (RYE).//P25877

F-PLACE4000392//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HE  
ME SYNTHETASE) (FRAGMENT).//0.91:36:50//YERSINIA PSEUDOTUBERCULOSIS.//Q0  
5338

F-PLACE4000401//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.4e-29:96:67/

/HOMO SAPIENS (HUMAN).//P39194

F-PLACE4000411//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.3e-18:41:73//

● HOMO SAPIENS (HUMAN).//P39188

F-PLACE4000431//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-).//5.4e-21:2  
37:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32639

F-PLACE4000445//HYPOTHETICAL 99.7 KD PROTEIN IN SDL1 5' REGION PRECURSOR.  
//0.00081:210:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40442

F-PLACE4000450//TRANSCRIPTION FACTOR HBP-1A (HISTONE-SPECIFIC TRANSCRIPT  
ION FACTOR HBP1).//0.020:87:33//TRITICUM AESTIVUM (WHEAT).//P23922

F-PLACE4000465//METALLOTHIONEIN-1L (MT-1L) (MT1X).//0.20:18:38//HOMO SAP  
IENS (HUMAN).//P80297

F-PLACE4000487//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.5e-19:73:52//

● HOMO SAPIENS (HUMAN).//P39188

F-PLACE4000489

F-PLACE4000494//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//0.17:130:3  
0//MUS MUSCULUS (MOUSE).//Q03173

F-PLACE4000521//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR  
ANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] (FRAGMENT).//3.0e-05:50:36//MUS  
MUSCULUS (MOUSE).//P10400

F-PLACE4000522//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR.//1.8  
e-45:231:47//RATTUS NORVEGICUS (RAT).//Q07008

F-PLACE4000548//CYTOCHROME C-551 (C551).//0.96:50:34//ECTOTHIORHODOSPIRA

HALOPHILA.//P00122

F-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING ENZYME FAF) (FAT FACETS PROTEIN).//1.6e-28:223:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P55824

F-PLACE4000581//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM) (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).//9.7e-11:166:28//HOMO SAPIENS (HUMAN).//P16109

F-PLACE4000590//POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.6e-17:134:35//GIBBON APE LEUKEMIA VIRUS.//P21414

F-PLACE4000593//GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R).//1.0:54:29//RATTUS NORVEGICUS (RAT).//P30969

F-PLACE4000612//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30].//2.6e-14:221:32//MOLONEY MURINE SARCOMA VIRUS (STRAIN TS110).//P32594

F-PLACE4000638//HYPOTHETICAL 9.3 KD PROTEIN IN NRDB-INAA INTERGENIC REGION.//0.65:37:40//ESCHERICHIA COLI.//P37910

F-PLACE4000650//ZINC FINGER PROTEIN 16 (ZINC FINGER PROTEIN KOX9) (FRAGMENT).//1.0:33:33//HOMO SAPIENS (HUMAN).//P17020

F-PLACE4000654

F-PLACE4000670//HYPOTHETICAL 44.1 KD PROTEIN IN RPB5-CDC28 INTERGENIC REGION.//1.6e-07:161:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33313

F-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//7.4e-15:223:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//060100

F-SKNMC1000013//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).//0.0013:128:35//GALLUS GALLUS (CHICKEN).//Q98937

F-SKNMC1000046//CUTICLE COLLAGEN 1.//0.0010:154:33//CAENORHABDITIS ELEGANS

NS./P08124

F-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE).//3.2e-41:87:98//HOMO SAPIENS (HUMAN).//P17655

F-SKNMC1000091//NTAK PROTEIN (NEURAL- AND THYMUS- DERIVED ACTIVATOR FOR ERBB KINASES).//0.0032:154:35//HOMO SAPIENS (HUMAN).//014511

F-THYRO1000017//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).//1.6e-23:124:37//CAENORHABDITIS ELEGANS.//Q20939

F-THYRO1000026//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.0e-13:54:66//HOMO SAPIENS (HUMAN).//P39192

F-THYRO1000034//HYPOTHETICAL 10.4 KD PROTEIN.//0.16:44:34//HEPATITIS B VIRUS (SUBTYPE AYW).//P03163

F-THYRO1000035//CAMPATH-1 ANTIGEN PRECURSOR (CD52 ANTIGEN) (CDW52) (CAMBRIDGE PATHOLOGY 1 ANTIGEN).//0.83:59:37//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//P32763

F-THYRO1000040//60S RIBOSOMAL PROTEIN L37 (FRAGMENT).//0.25:23:39//BOS TAURUS (BOVINE).//P79244

F-THYRO1000070//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//2.3e-11:133:36//0RGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//010341

F-THYRO1000072//C-PROTEIN, SKELETAL MUSCLE SLOW-ISOFORM.//1.5e-14:205:29//HOMO SAPIENS (HUMAN).//Q00872

F-THYRO1000085

F-THYRO1000092//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.063:59:33//HOMO SAPIENS (HUMAN).//P49901

F-THYRO1000107

F-THYRO1000111//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-58:110:67//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-THYRO1000121//SPLICOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//2.6e-06:134:35//MUS MUSCULUS (MOUSE).//Q62203

F-THYR01000124//TENECIN 3 PRECURSOR.//0.047:76:35//TENEBRIO MOLITOR (YELLOW MEALWORM).//Q27270

F-THYR01000129//FIBROSIN (FRAGMENT).//0.35:43:34//MUS MUSCULUS (MOUSE).//Q60791

F-THYR01000132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//8.7e-14:104:42//HOMO SAPIENS (HUMAN).//P39188

F-THYR01000156

F-THYR01000163//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//3.7e-20:71:71//HOMO SAPIENS (HUMAN).//P39189

F-THYR01000173//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//6.7e-88:216:76//MUS MUSCULUS (MOUSE).//P35585

F-THYR01000186//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//2.9e-24:72:77//HOMO SAPIENS (HUMAN).//P39192

F-THYR01000187

F-THYR01000190//PROTEIN TRANSPORT PROTEIN SEC61 BETA 2 SUBUNIT.//0.060:50:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52871

F-THYR01000197

F-THYR01000199//HYPOTHETICAL 49.8 KD PROTEIN D2007.5 IN CHROMOSOME III.//2.0e-06:88:35//CAENORHABDITIS ELEGANS.//P34379

F-THYR01000206

F-THYR01000221

F-THYR01000241//HYPOTHETICAL 11.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION.//1.0:51:35//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNP V).//P41661

F-THYR01000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//7.4e-37:137:36//HOMO SAPIENS (HUMAN).//P51523

F-THYR01000253//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)

./.0.11:21:52//HOMO SAPIENS (HUMAN).//P30808

F-THYR01000270//WDNM1 PROTEIN PRECURSOR./.0.40:52:32//MUS MUSCULUS (MOUSE).//Q62477

F-THYR01000279//BETA CRYSTALLIN A4./.0.97:64:26//BOS TAURUS (BOVINE).//P11842

F-THYR01000288//POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1) (PPSEP 1).//3.4e-48:142:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10071

F-THYR01000320//ZINC FINGER PROTEIN 14 (ZFP-14) (KROX-9 PROTEIN) (FRAGMENT).//0.87:35:45//MUS MUSCULUS (MOUSE).//P10755

F-THYR01000327//HYPOTHETICAL 64.7 KD PROTEIN F26E4.11 IN CHROMOSOME I./.0.00010:75:26//CAENORHABDITIS ELEGANS.//P90859

F-THYR01000343//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN; BETA-GRANIN; WE-14].//0.88:107:26//MUS MUSCULUS (MOUSE).//P26339

F-THYR01000358//SELENIUM-BINDING LIVER PROTEIN./.4.6e-25:49:81//MUS MUSCULUS (MOUSE).//P17563

F-THYR01000368//LOCOMOTION-RELATED PROTEIN HIKARU GENKI PRECURSOR./.1.0:136:26//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09101

F-THYR01000381//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10].//0.032:99:35//SIMIAN SARCOMA VIRUS.//P03330

F-THYR01000387//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.90:46:30//HALICHOERUS GRYPUS (GRAY SEAL).//P38592

F-THYR01000394//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0019:48:37//HOMO SAPIENS (HUMAN).//P22531

F-THYR01000395//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-33:186:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-THYR01000401//50S RIBOSOMAL PROTEIN L7/L12 (FRAGMENT).//0.57:67:31//STAPHYLOCOCCUS AUREUS.//P48860

F-THYR01000438//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:38//

STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P15997

F-THYR01000452//BACTERIOCIN CARNOBACTERIOCIN A PRECURSOR (PISCICOLIN 61)

.//0.31:34:44//CARNOBACTERIUM PISCICOLA.//P38578

F-THYR01000471//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.1e-31:94:72/

/HOMO SAPIENS (HUMAN).//P39194

F-THYR01000484//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//5.9e-08:30:86/

/HOMO SAPIENS (HUMAN).//P39195

F-THYR01000488//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.

93:98:27//GLYCINE MAX (SOYBEAN).//Q02917

F-THYR01000501//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//2.4e

-51:198:50//MUS MUSCULUS (MOUSE).//P15533

F-THYR01000502//HUNCHBACK PROTEIN (FRAGMENT).//0.84:41:43//APIS MELLIFER

A (HONEYBEE).//P31504

F-THYR01000505//HYPOTHETICAL BHLF1 PROTEIN.//0.99:231:33//EPSTEIN-BARR V

IRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-THYR01000558//ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).//0.47:58:

37//GALLUS GALLUS (CHICKEN).//Q03352

F-THYR01000569//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00048:64:42//R

ATTUS NORVEGICUS (RAT).//P02454

F-THYR01000570//HYPOTHETICAL 11.6 KD PROTEIN IN ACS1-GCV3 INTERGENIC REG

ION.//0.94:61:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39725

F-THYR01000585//SPLICING FACTOR, ARGININE/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR SRP55).//0.050:104:36//HOMO SAPIENS (HUMAN).//Q13247

F-THYR01000596//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP 34.5).//0.99:37:40//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10).//P373

19

F-THYR01000602//EAMZP30-47 PROTEIN (FRAGMENT).//0.88:61:34//EIMERIA ACER VULINA.//P21959

F-THYRO1000605//SUPPRESSOR PROTEIN SRP40.//0.0016:116:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

F-THYRO1000625//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.4e-33:88:78//HOMO SAPIENS (HUMAN).//P39194

F-THYRO1000637//METALLOTHIONEIN A (MT A).//1.0:23:43//SPARUS AURATA (GIL THEAD SEA BREAM).//P52727

F-THYRO1000641//PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN.//0.99:26:46//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//019925

F-THYRO1000658//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.5e-49:116:69//HOMO SAPIENS (HUMAN).//P39189

F-THYRO1000662//DNA-DAMAGE-INDUCIBLE PROTEIN P.//3.7e-15:119:43//ESCHERICHIA COLI.//Q47155

F-THYRO1000666//KINESIN-LIKE PROTEIN KLP1.//1.0e-44:232:41//CHLAMYDOMONAS REINHARDTII.//P46870

F-THYRO1000676//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//2.1e-15:144:39//HOMO SAPIENS (HUMAN).//P39193

F-THYRO1000684//HYPOTHETICAL 73.5 KD PROTEIN IN SCS3-RPS2 INTERGENIC REGION.//0.00033:84:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53129

F-THYRO1000699//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//0.97:20:85//HOMO SAPIENS (HUMAN).//P39192

F-THYRO1000712//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.2e-10:69:59//HOMO SAPIENS (HUMAN).//P39188

F-THYRO1000715//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.6e-10:204:32//HOMO SAPIENS (HUMAN).//P04280

F-THYRO1000734

F-THYRO1000748//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8e-46:130:7//HOMO SAPIENS (HUMAN).//043295

F-THYRO1000756//ALPHA-N-ACETYLGLACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERAS

E (EC 2.4.99.-) (ST6GALNACIII) (STY).//1.1e-06:95:31//RATTUS NORVEGICUS  
(RAT).//Q64686

F-THYR01000777//CUTICLE COLLAGEN 2C (FRAGMENT).//0.0031:119:34//HAEMONCHUS  
US CONTORTUS.//P16252

F-THYR01000783//MYOSIN IC HEAVY CHAIN.//0.0014:121:37//ACANTHAMOEBA CASTELLANII  
(AMOEBA).//P10569

F-THYR01000787//HUNCHBACK PROTEIN (FRAGMENT).//0.54:25:52//PHOLCUS PHALANGIOIDES  
//Q02031

F-THYR01000793//PRE-MRNA SPLICING FACTOR PRP9.//0.91:30:36//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST).//P19736

F-THYR01000796

F-THYR01000805//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//0  
.081:31:38//HUMAN ADENOVIRUS TYPE 41.//P23691

F-THYR01000815//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//6.0e-30:81:70/  
/HOMO SAPIENS (HUMAN).//P39195

F-THYR01000829//NEUROTOXIN III (BOM III).//0.022:32:34//BUTHUS OCCITANUS  
MARDOCHEI (MOROCCAN SCORPION).//P13488

F-THYR01000843//HYPOTHETICAL 7.7 KD PROTEIN IN GENES 5-4 INTERGENIC REGION  
(ORF 109).//0.98:25:44//BACTERIOPHAGE P22.//P26750

F-THYR01000852//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//7.3e-09:83  
:42//VOLVOX CARTERI.//P21997

F-THYR01000855//ANTIFREEZE PEPTIDE 4 PRECURSOR.//1.0:54:35//PSEUDOPLEURONECTA  
AMERICANUS (WINTER FLOUNDER).//P02734

F-THYR01000865//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.2e-17:66:57//  
HOMO SAPIENS (HUMAN).//P39188

F-THYR01000895//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.0e-12:58:62/  
/HOMO SAPIENS (HUMAN).//P39189

F-THYR01000916//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.0e-32:101:69  
//HOMO SAPIENS (HUMAN).//P39189

F-THYR01000926//NITROGEN FIXATION REGULATORY PROTEIN.//5.5e-05:108:27//K  
LEBSIELLA OXYTOCA.//P56267

F-THYR01000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P  
5C REDUCTASE).//3.9e-50:147:40//HOMO SAPIENS (HUMAN).//P32322

F-THYR01000951//DIHYDROXYACETONE KINASE (EC 2.7.1.29) (GLYCERONE KINASE)  
.//1.8e-31:136:56//CITROBACTER FREUNDII.//P45510

F-THYR01000952//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC RE  
GION.//2.4e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170

F-THYR01000974//MITOCHONDRIAL ATP-DEPENDENT RNA HELICASE SUV3 PRECURSOR.  
.//1.0:35:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32580

F-THYR01000975

F-THYR01000983//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//1  
.3e-20:96:51//CAENORHABDITIS ELEGANS.//Q11076

F-THYR01000984//GTP-BINDING ADP-RIBOSYLATION FACTOR HOMOLOG 1 PROTEIN.//  
0.011:76:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25160

F-THYR01000988

F-THYR01001003//HYPOTHETICAL 8.1 KD PROTEIN IN MSCL-RPLQ INTERGENIC REGI  
ON.//0.97:60:31//ESCHERICHIA COLI.//P36675

F-THYR01001031//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//9.5e-18:56:66/  
.//HOMO SAPIENS (HUMAN).//P39195

F-THYR01001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//5.0e-13:  
126:35//HOMO SAPIENS (HUMAN).//P31948

F-THYR01001062//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.1e-35:97:79/  
.//HOMO SAPIENS (HUMAN).//P39194

F-THYR01001093//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//6.4e-13:70:57/  
.//HOMO SAPIENS (HUMAN).//P39194

F-THYR01001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//4.2e-63:2  
19:63//HOMO SAPIENS (HUMAN).//P98168

F-THYR01001120//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.

00068:160:31//HOMO SAPIENS (HUMAN).//Q15427

F-THYR01001121//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME  
I.//0.37:158:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10263

F-THYR01001133//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//7.3e-15:59:66//  
HOMO SAPIENS (HUMAN).//P39188

F-THYR01001134//SALIVARY PROLINE-RICH PROTEIN P0 (ALLELE M) [CONTAINS: P  
EPTIDE P-D] (FRAGMENT).//0.00088:159:29//HOMO SAPIENS (HUMAN).//P10161

F-THYR01001142//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.0e-29:81:71//  
HOMO SAPIENS (HUMAN).//P39194

F-THYR01001173//CYTOCHROME C OXIDASE POLYPEPTIDE VIIS (EC 1.9.3.1).//0.8  
8:51:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P20610

F-THYR01001177//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.0e-24:91:68//  
HOMO SAPIENS (HUMAN).//P39192

F-THYR01001189//MKR2 PROTEIN (ZINC FINGER PROTEIN 2).//7.3e-27:165:39//M  
US MUSCULUS (MOUSE).//P08043

F-THYR01001204//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.67:42:42//HOMO  
SAPIENS (HUMAN).//P02811

F-THYR01001213//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.9e-16:61:68//  
HOMO SAPIENS (HUMAN).//P39194

F-THYR01001262//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.4e-36:50:84//  
HOMO SAPIENS (HUMAN).//P39193

F-THYR01001271//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.62  
:126:30//STREPTOMYCES FRADIAE.//P20186

F-THYR01001287//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC RE  
GION.//1.9e-26:208:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38888

F-THYR01001290//GIANT HEMOGLOBIN AIV CHAIN (FRAGMENT).//1.0:31:38//LAMEL  
LIBRACHIA SP. (DEEP-SEA GIANT TUBE WORM).//P20413

F-THYR01001313//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//0.000  
42:105:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331

F-THYR01001320//COLLAGEN ALPHA 1(III) CHAIN.//0.27:57:38//BOS TAURUS (BOVINE).//P04258

F-THYR01001321//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.5e-20:74:64//HOMO SAPIENS (HUMAN).//P39188

F-THYR01001322//HYPOTHETICAL 7.2 KD PROTEIN.//0.66:49:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21123

F-THYR01001347//TOXIN F-VIII PRECURSOR (TOXIN TA2) (TOXIN DAF8).//0.94:61:36//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P01404

F-THYR01001363//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.0025:23:73//HOMO SAPIENS (HUMAN).//P39188

F-THYR01001365//MERSACIDIN PRECURSOR.//0.35:38:42//BACILLUS SP. (STRAIN HIL-Y85/54728).//P43683

F-THYR01001374//PROTEIN VDLD.//1.6e-13:140:31//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//005729

F-THYR01001401//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//0.047:43:48//HOMO SAPIENS (HUMAN).//P39192

F-THYR01001403

F-THYR01001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.068:26:42//HOMO SAPIENS (HUMAN).//P22531

F-THYR01001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//3.1e-81:97:83//MUS MUSCULUS (MOUSE).//070503

F-THYR01001411//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.9e-26:89:74//HOMO SAPIENS (HUMAN).//P39193

F-THYR01001426//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.4e-09:55:61//HOMO SAPIENS (HUMAN).//P39193

F-THYR01001434//BETA-DEFENSIN 4 PRECURSOR (BNDB-4).//0.68:44:34//BOS TAURUS (BOVINE).//P46162

F-THYR01001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//3.8e-64:216:62//HOMO SAPIENS (HUMAN).//P3

5580

F-THYR01001480//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.3e-29:88:75/  
/HOMO SAPIENS (HUMAN).//P39194

F-THYR01001487//HOMEobox PROTEIN HOX-B4 (HOX-2.6).//0.99:59:37//MUS MUSC  
ULUS (MOUSE).//P10284

F-THYR01001534//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.4e-14:40:82/  
/HOMO SAPIENS (HUMAN).//P39194

F-THYR01001537//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FL05 INTERGENIC REG  
ION.//2.4e-07:142:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38892

F-THYR01001541//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.98:26:61//HO  
MO SAPIENS (HUMAN).//P39195

F-THYR01001559//PROTEIN Q300.//2.6e-05:20:75//MUS MUSCULUS (MOUSE).//Q02  
722

F-THYR01001570

F-THYR01001573//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.033:  
71:36//MUS MUSCULUS (MOUSE).//P15265

F-THYR01001584//SUPPRESSOR PROTEIN SRP40.//2.1e-05:188:27//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST).//P32583

F-THYR01001595//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)  
.//6.1e-21:35:91//HOMO SAPIENS (HUMAN).//Q15404

F-THYR01001602//TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKH.//1.0:57:42//HA  
EMOPHILUS INFLUENZAE.//P44843

F-THYR01001605//VENOM BASIC PROTEASE INHIBITORS IX AND VIIIB.//1.0:34:38  
//BUNGARUS FASCIATUS (BANDED KRAIT).//P25660

F-THYR01001617//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.0e-18:55:81/  
/HOMO SAPIENS (HUMAN).//P39194

F-THYR01001637//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.00020:25:80/  
/HOMO SAPIENS (HUMAN).//P39195

F-THYR01001656//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.0091:54:42//MUS

MUSCULUS (MOUSE).//P05142

F-THYR01001661//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGION (0182).//0.033:77:35//ESCHERICHIA COLI.//P09160

F-THYR01001671//(2'-5')OLIGOADENYLATE SYNTHETASE 1 (EC 2.7.7.-) ((2-5')OLIGO(A) SYNTHETASE 1) (2-5A SYNTHETASE 1) (P46/P41) (E18/E16).//4.3e-34:207:34//HOMO SAPIENS (HUMAN).//P00973

F-THYR01001673//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.9e-08:49:65//HOMO SAPIENS (HUMAN).//P39194

F-THYR01001703//HYPOTHETICAL 69.8 KD PROTEIN IN BDF1-SFP1 INTERGENIC REGION.//6.4e-16:134:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06053

F-THYR01001706

F-THYR01001721//RING CANAL PROTEIN (KELCH PROTEIN).//2.7e-27:191:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-THYR01001738//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE A INTERFERENCE PROTEIN).//0.0032:105:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027

F-THYR01001745

F-THYR01001746//GENE 10 PROTEIN.//1.0:55:30//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15901

F-THYR01001772//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.2e-05:41:63//HOMO SAPIENS (HUMAN).//P39188

F-THYR01001793//HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III.//1.5e-26:161:42//CAENORHABDITIS ELEGANS.//P41880

F-THYR01001809//LATENCY-RELATED PROTEIN 2.//0.49:74:27//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN F).//P17589

F-THYR01001828//PROTEINASE INHIBITOR.//0.11:34:50//SOLANUM MELONGENA (EGGPLANT) (AUBERGINE).//P01078

F-THYR01001854//ACYL-COA-BINDING PROTEIN HOMOLOG (ACBP) (DIAZEPAM BINDING INHIBITOR HOMOLOG) (DBI).//0.63:50:38//RANA RIDIBUNDA (LAUGHING FROG)

(MARSH FROG).//P45883

F-THYR01001895//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//6.1e-09:72:47//  
HOMO SAPIENS (HUMAN).//P39188

F-THYR01001907//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGME  
NT).//0.79:36:44//TRYPANOSOMA CRUZI.//Q26327

F-VESEN1000122//HOMEobox PROTEIN HB9.//0.57:64:32//HOMO SAPIENS (HUMAN).  
//P50219

F-Y79AA1000013//METALLOTHIONEIN B (MT-B).//0.034:35:48//SALMO SALAR (ATL  
ANTIC SALMON).//P52720

F-Y79AA1000033//CHOLECYSTOKININ.//0.97:49:30//PSEUDEMYS SCRIPTA (SLIDER  
TURTLE).//P80345

F-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//1.4e-23:80:60//HOMO SAPIENS  
(HUMAN).//P35226

F-Y79AA1000059//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00  
75:127:36//STREPTOMYCES FRADIAE.//P20186

F-Y79AA1000065//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: P  
EPTIDE P-D] (FRAGMENT).//0.022:135:29//HOMO SAPIENS (HUMAN).//P10162

F-Y79AA1000131//REGULATORY PROTEIN E2.//1.1e-05:175:26//HUMAN PAPILLOMAV  
IRUS TYPE 24.//P50770

F-Y79AA1000181//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.4e-06:187:29//M  
US MUSCULUS (MOUSE).//P05143

F-Y79AA1000202//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//6.2e-09:4  
7:53//OWENIA FUSIFORMIS.//P21260

F-Y79AA1000214//HISTONE H2A VARIANT.//1.7e-50:107:100//GALLUS GALLUS (CH  
ICKEN).//P02272

F-Y79AA1000230//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE  
RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBE  
RIN I).//0.27:64:34//HOMO SAPIENS (HUMAN).//P01148

F-Y79AA1000231//HYPOTHETICAL 47.9 KD PROTEIN M021B04.12.//2.5e-72:277:53

//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//004658

F-Y79AA1000258//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//2.8e-08:174:35//MUS MUSCULUS (MOUSE).//P05142

F-Y79AA1000268//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.00020:176:33//RATTUS NORVEGICUS (RAT).//P13941

F-Y79AA1000313//HYPOTHETICAL 54.0 KD PROTEIN C32A3.1 IN CHROMOSOME III.//0.092:127:21//CAENORHABDITIS ELEGANS.//Q09260

F-Y79AA1000328//SEL-10 PROTEIN.//5.3e-05:129:28//CAENORHABDITIS ELEGANS.//Q93794

F-Y79AA1000342//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//1.0:73:30//OVIS ARIES (SHEEP).//P26372

F-Y79AA1000346//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.8e-95:205:83//BOS TAURUS (BOVINE).//P53620

F-Y79AA1000349//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.036:37:54//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER).//P02734

F-Y79AA1000355//HYPOTHETICAL 18.2 KD PROTEIN ZK632.13 IN CHROMOSOME III.//0.0031:106:28//CAENORHABDITIS ELEGANS.//Q10120

F-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.4e-16:208:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25343

F-Y79AA1000405//LIGHT-HARVESTING PROTEIN B-800-850, ALPHA CHAIN C (ANTENNA PIGMENT PROTEIN, ALPHA CHAIN C) (LH II-C ALPHA).//0.98:50:30//RHODOPSEUDOMONAS PALUSTRIS.//P35103

F-Y79AA1000410//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.9e-20:62:79//HOMO SAPIENS (HUMAN).//P39194

F-Y79AA1000420//HYPOTHETICAL 27.7 KD PROTEIN IN UME3-HDA1 INTERGENIC REGION.//1.4e-06:86:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53970

F-Y79AA1000469//HYPOTHETICAL 48.4 KD PROTEIN F44B9.5 IN CHROMOSOME III.//2.8e-34:211:40//CAENORHABDITIS ELEGANS.//P34426

F-Y79AA1000480//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I.//3

.9e-15:90:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10414

F-Y79AA1000538//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.37:41:48//HOMO SAPIENS (HUMAN).//P39195

F-Y79AA1000539//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.8e-21:190:37//HOMO SAPIENS (HUMAN).//Q08170

F-Y79AA1000540//SPERM PROTAMINE P1.//0.00045:66:45//DASYURUS VIVERRINUS (SOUTHEASTERN QUOLL), AND DASYURUS HALLUCATUS.//P42135

F-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTER HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.6e-79:186:87//MUS MUSCULUS (MOUSE).//P17427

F-Y79AA1000574//AKLAVINONE C-11 HYDROXYLASE (EC 1.---) (FRAGMENT).//0.010:35:60//STREPTOMYCES PEUCETIUS.//P32009

F-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//4.5e-27:197:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28320

F-Y79AA1000627//ZINC FINGER PROTEIN 134.//1.6e-34:191:35//HOMO SAPIENS (HUMAN).//P52741

F-Y79AA1000705//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION.//8.7e-36:250:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P31380

F-Y79AA1000734//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN-11A).//0.00037:108:27//CANDIDA BOIDINII (YEAST).//Q00316

F-Y79AA1000748//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III.//1.0e-23:210:34//CAENORHABDITIS ELEGANS.//Q09316

F-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRN P X) (CBP).//1.4e-53:156:68//MUS MUSCULUS (MOUSE).//Q61990

F-Y79AA1000774//HYPOTHETICAL 77.9 KD PROTEIN IN RRN10-MCM2 INTERGENIC REGION.//1.2e-11:231:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38205

F-Y79AA1000782//CUTICLE COLLAGEN 2.//0.012:56:35//CAENORHABDITIS ELEGANS

./P17656

F-Y79AA1000784//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.3e-08:82:39//P  
LASMODIUM LOPHURAE.//P04929

F-Y79AA1000794//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
./.0.043:13:53//HOMO SAPIENS (HUMAN).//P30808

F-Y79AA1000800//PRIA PROTEIN PRECURSOR.//0.031:94:34//LENTINULA EDODES (SHIITAKE MUSHROOM) (LENTINUS EDODES).//Q01200

F-Y79AA1000802//HYPOTHETICAL 67.4 KD PROTEIN IN RPS3-PSD1 INTERGENIC REGION.//0.26:186:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53882

F-Y79AA1000805//AMP DEAMINASE (EC 3.5.4.6) (MYOADENYLATE DEAMINASE).//0.99:78:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P50998

F-Y79AA1000824//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REGION.//3.4e-44:111:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48234

F-Y79AA1000827//HYPOTHETICAL BHLF1 PROTEIN.//0.0046:187:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//1.0e-75:239:66//CRICETULUS GRISEUS (CHINESE HAMSTER).//P05209

F-Y79AA1000850//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.0078:57:31//HOMO SAPIENS (HUMAN).//P22532

F-Y79AA1000962//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//8.5e-11:241:26//GALLUS GALLUS (CHICKEN).//P10587

F-Y79AA1000966//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.69:12:31//TRYPANOSOMA BRUCEI BRUCEI.//P24499

F-Y79AA1000968//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).//3.3e-102:211:93//RATTUS NORVEGICUS (RAT).//P70541

F-Y79AA1000969//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:67:38//GALLUS GALLUS (CHICKEN).//P02457

F-Y79AA1000976//INVOLUCRIN.//0.99:66:31//CEBUS ALBIFRONS (WHITE-FRONTED

CAPUCHIN).//P24709

F-Y79AA1000985//PERICENTRIN.//1.1e-24:116:59//MUS MUSCULUS (MOUSE).//P48  
725

F-Y79AA1001023//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC RE  
GION.//0.37:79:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38250

F-Y79AA1001041//SPERMATID-SPECIFIC PROTEIN T1 [CONTAINS: SPERM PROTAMINE  
SP1].//0.93:43:39//SEPIA OFFICINALIS (COMMON CUTTLEFISH).//P80001

F-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURS  
OR (EC 1.3.99.-) (VLCAD).//1.5e-51:211:52//BOS TAURUS (BOVINE).//P48818

F-Y79AA1001061//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.8e-25:85:69/  
/HOMO SAPIENS (HUMAN).//P39194

F-Y79AA1001068//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHOND  
ROCALCIN].//0.0015:207:33//MUS MUSCULUS (MOUSE).//P28481

F-Y79AA1001077//ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 11.9 (ACP 11.9)./  
/0.99:36:41//ARANEUS DIADEMATUS (SPIDER).//P80515

F-Y79AA1001078//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III.  
//1.0e-06:197:23//CAENORHABDITIS ELEGANS.//P34492

F-Y79AA1001105//HOMEobox PROTEIN OTX2.//2.9e-62:163:79//MUS MUSCULUS (MO  
USE).//P80206

F-Y79AA1001145//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.024:42:59//H  
OMO SAPIENS (HUMAN).//P39195

F-Y79AA1001167//HYPOTHETICAL 7.1 KD PROTEIN IN IAP2-VLF1 INTERGENIC REGI  
ON.//0.96:20:50//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMN  
PV).//P41471

F-Y79AA1001177//HYPOTHETICAL BHLF1 PROTEIN.//3.9e-05:135:34//EPSTEIN-BAR  
R VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-Y79AA1001185//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.00017:93:38//CAENO  
RHABDITIS ELEGANS.//Q09456

F-Y79AA1001211

F-Y79AA1001216//TENSIN.//0.012:134:32//GALLUS GALLUS (CHICKEN).//Q04205

F-Y79AA1001228//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.088:75:34//HOMO SAPIENS (HUMAN).//Q02817

F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 1).//1.1e-40:139:51//RATTUS NORVEGICUS (RAT).//P51657

F-Y79AA1001236//HYPOTHETICAL 34.7 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.//2.0e-22:108:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38238

F-Y79AA1001281

F-Y79AA1001299//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0022:49:44//MUS MUSCULUS (MOUSE).//P05143

F-Y79AA1001312//50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR.//0.98:117:25//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P92959

F-Y79AA1001323//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//0.082:44:40//SUS SCROFA (PIG).//P35323

F-Y79AA1001384//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.99:47:40//MUS MUSCULUS (MOUSE).//P33622

F-Y79AA1001391//HOMEobox PROTEIN HOX-A13 (HOX-1J).//9.8e-58:157:62//HOMO SAPIENS (HUMAN).//P31271

F-Y79AA1001394//TRICHOHYALIN.//4.7e-08:121:36//HOMO SAPIENS (HUMAN).//Q07283

F-Y79AA1001402//ETS-DOMAIN TRANSCRIPTION FACTOR ERF.//0.0087:81:33//MUS MUSCULUS (MOUSE).//P70459

F-Y79AA1001493//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//4.5e-21:125:44//CAENORHABDITIS ELEGANS.//Q11076

F-Y79AA1001511//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION.//2.3e-17:249:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53313

F-Y79AA1001533//DNA-DIRECTED RNA POLYMERASE I 49 KD POLYPEPTIDE (EC 2.7.

7.6) (A49).//0.0099:155:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q

01080

F-Y79AA1001541

F-Y79AA1001548//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.1e-17:53:83/

/HOMO SAPIENS (HUMAN).//P39192

F-Y79AA1001555//MAJOR SURFACE ANTIGEN.//0.046:62:29//HEPATITIS B VIRUS./  
/P31873

F-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA  
LIGASE) (ACYL- ACTIVATING ENZYME).//8.6e-11:144:31//ESCHERICHIA COLI.//P

27550

F-Y79AA1001585//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.012:  
64:40//MUS MUSCULUS (MOUSE).//P15265

F-Y79AA1001594//CORNIFIN BETA.//0.61:88:31//MUS MUSCULUS (MOUSE).//00911  
6

F-Y79AA1001603//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TA  
FII-135) (TAFII135) (TAFII-130) (TAFII130).//0.024:170:30//HOMO SAPIENS  
(HUMAN).//000268

F-Y79AA1001613//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1)./  
/4.5e-09:136:27//HOMO SAPIENS (HUMAN).//P28698

F-Y79AA1001647//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C.//0.093:94:26//MY  
COBACTERIUM TUBERCULOSIS.//P71779

F-Y79AA1001665//HOMEobox PROTEIN DLX-2 (HOMEobox PROTEIN TES-1).//0.79:9  
0:26//MUS MUSCULUS (MOUSE).//P40764

F-Y79AA1001679//LAMBDA-CRYSTALLIN.//1.6e-95:224:81//ORYCTOLAGUS CUNICULU  
S (RABBIT).//P14755

F-Y79AA1001692//GERM CELL-LESS PROTEIN.//3.5e-08:78:38//DROSOPHILA MELAN  
OGASTER (FRUIT FLY).//Q01820

F-Y79AA1001696//INSULIN.//1.0:33:27//ANGUILLA ROSTRATA (AMERICAN EEL).//  
P42633

F-Y79AA1001705//HYPOTHETICAL BHLF1 PROTEIN.//0.0013:192:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-Y79AA1001711//PARATHYMOSEN (ZINC-BINDING 11.5 KD PROTEIN).//0.032:38:34//RATTUS NORVEGICUS (RAT).//P04550

F-Y79AA1001781

F-Y79AA1001805//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0063:128:30//HOMO SAPIENS (HUMAN).//P50552

F-Y79AA1001827//SPERM PROTAMINE P1.//0.015:45:40//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305

F-Y79AA1001846//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-09:42:73//HOMO SAPIENS (HUMAN).//P39188

F-Y79AA1001848//KRUEPPEL PROTEIN (FRAGMENT).//1.8e-10:63:44//PSYCHODA CINEREA.//Q02035

F-Y79AA1001866//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//0.00036:108:37//MUS MUSCULUS (MOUSE).//Q61967

F-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPT IONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//3.2e-07:100:35//HOMO SAPIENS (HUMAN).//P43489

F-Y79AA1001875//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.020:25:64//HOMO SAPIENS (HUMAN).//P20931

F-Y79AA1001923//SALIVARY PROLINE-RICH PROTEIN P0 (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.016:83:36//HOMO SAPIENS (HUMAN).//P10162

F-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//8.1e-13:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//042643

F-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.8e-39:143:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743

F-Y79AA1002083//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)

.//0.036:53:45//HOMO SAPIENS (HUMAN).//P30808

F-Y79AA1002089//HYPOTHETICAL 49.1 KD PROTEIN F02A9.4 IN CHROMOSOME III.//

/0.12:171:22//CAENORHABDITIS ELEGANS.//P34384

F-Y79AA1002093//MAX PROTEIN.//3.1e-07:111:29//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//P52161

F-Y79AA1002103//SHORT NEUROTOXIN C.//0.040:21:47//AIPYSURUS LAEVIS (OLIVE SEA SNAKE).//P19958

F-Y79AA1002115//HYPOTHETICAL PROTEIN MJ0827.//0.84:68:30//METHANOCOCCUS JANNASCHII.//Q58237

F-Y79AA1002125//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC REGION.//3.4e-29:197:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40206

F-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//1.9e-19:120:45//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24133

F-Y79AA1002204//TBX6 PROTEIN (T-BOX PROTEIN 6).//0.0011:162:32//MUS MUSCULUS (MOUSE).//P70327

F-Y79AA1002208//ANKYRIN.//2.9e-08:231:29//MUS MUSCULUS (MOUSE).//Q02357

F-Y79AA1002209//TYROSYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRRS).//3.7e-23:170:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48527

F-Y79AA1002210//CORNIFIN A (SMALL PROLINE-RICH PROTEIN IA) (SPR-IA) (SPRK).//0.0061:69:31//HOMO SAPIENS (HUMAN).//P35321

F-Y79AA1002211//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//9.2e-10:43:62//HOMO SAPIENS (HUMAN).//P39193

F-Y79AA1002220

F-Y79AA1002229//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I.//1.9e-21:147:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264

F-Y79AA1002234

F-Y79AA1002246//MYOSIN IC HEAVY CHAIN.//0.00066:131:34//ACANTHAMOEBA CAS TELLANII (AMOEBA).//P10569

F-Y79AA1002258//HYPOTHETICAL 103.9 KD PROTEIN ZK370.3 IN CHROMOSOME III. //4.3e-45:164:48//CAENORHABDITIS ELEGANS.//Q02328

F-Y79AA1002298//SALIVARY PROLINE-RICH PROTEIN PO (ALLEL M) [CONTAINS: P EPTIDE P-D] (FRAGMENT).//0.0063:99:31//HOMO SAPIENS (HUMAN).//P10161

F-Y79AA1002307

F-Y79AA1002311//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III. //0.75:198:24//CAENORHABDITIS ELEGANS.//P46012

● F-Y79AA1002351//CUTICLE COLLAGEN 34.//0.74:128:35//CAENORHABDITIS ELEGANS.//P34687

F-Y79AA1002361//GLC7-INTERACTING PROTEIN 2.//0.050:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40036

F-Y79AA1002399//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57).//1.0:89:30//CARASSIUS AURATUS (GOLDFISH).//P17691

F-Y79AA1002407//HYPOTHETICAL 31.5 KD PROTEIN IN YGP1-YCK2 INTERGENIC REGION.//3.7e-16:232:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53899

● F-Y79AA1002416//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//6.7e-72:162:84//HOMO SAPIENS (HUMAN).//P17812

F-Y79AA1002431//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.8 1:34:41//HOMO SAPIENS (HUMAN).//P22531

F-Y79AA1002433//CELL DIVISION CONTROL PROTEIN 68.//0.00024:85:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32558

F-Y79AA1002472//ZINC FINGER PROTEIN 35 (ZFP-35).//2.3e-60:217:44//MUS MUSCULUS (MOUSE).//P15620

F-Y79AA1002482//ZINC FINGER PROTEIN 141.//2.0e-31:90:55//HOMO SAPIENS (HUMAN).//Q15928

F-Y79AA1002487//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN

C57A10.05C IN CHROMOSOME I.//0.18:41:36//SCHIZOSACCHAROMYCES POMBE (FISS  
ION YEAST).//P87053

【0832】

相同性検索結果データ2.

5'末端クローン配列に対するESTとSTSを除いたGenBank相同性検索結果データ

各データは

クローン配列名、

トップヒットデータのDefinition、

P値:比較配列の長さ (base):相同性(%)、

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、相同性のスコアのP値が1より大であった場合はデータは示さない。

F-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds  
././/3.4e-106:695:86//L16953

F-HEMBA1000012//Caenorhabditis elegans cosmid C16C10, complete sequence.  
//1.5e-24:374:66//Z46787

F-HEMBA1000020//Homo sapiens beta 2 gene.//3.5e-112:529:90//X02344

F-HEMBA1000030//Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein (GIT1) mRNA, complete cds.//5.6e-124:743:88//AF085693

F-HEMBA1000042//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-25:529:65//AC004581

F-HEMBA1000046//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 125I3, WORKING DRAFT SEQUENCE.//3.2e-11:330:63//AL033528

F-HEMBA1000050//Homo sapiens DNA sequence from PAC 172K10 on chromosome 6q24. Contains STS, GSS and chromosome 6 fragment, complete sequence.//0.32:407:59//AL022477

F-HEMBA1000076//Homo sapiens full length insert cDNA clone ZB97G06.//6.2e-135:594:98//AF086182

F-HEMBA1000111//CIT-HSP-2291M18.TF CIT-HSP Homo sapiens genomic clone 22

91M18, genomic survey sequence.//2.8e-16:132:79//AQ004134  
F-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//8.6e-98:230:93//AC003104  
F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//2.1e-167:791:98//AB018340  
F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds.//2.2e-44:242:96//AB018331  
F-HEMBA1000156//Rattus norvegicus scaffold attachment factor B mRNA, complete cds.//1.1e-10:409:60//AF056324  
● F-HEMBA1000158//Homo sapiens CAGH44 mRNA, partial cds.//1.6e-35:365:73//U80741  
F-HEMBA1000168//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING DRAFT SEQUENCE.//0.99:290:61//AL031033  
F-HEMBA1000180//rat u2 small nuclear rna gene and flanks.//3.7e-18:112:98//K00034  
F-HEMBA1000185  
F-HEMBA1000193//Human FMR1 gene, 5' end.//0.0012:191:67//L19476  
F-HEMBA1000201//Human In11 mRNA, complete cds.//2.0e-73:440:92//U04847  
● F-HEMBA1000213//Plasmodium falciparum MAL3P7, complete sequence.//0.90:32:59//AL034559  
F-HEMBA1000216//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//4.8e-117:585:83//AF060194  
F-HEMBA1000227//H.sapiens CpG island DNA genomic Mse1 fragment, clone 179h6, reverse read cpg179h6.rt1a.//1.9e-14:95:98//Z64921  
F-HEMBA1000231//H.sapiens CpG island DNA genomic Mse1 fragment, clone 90a5, reverse read cpg90a5.rt1a.//5.1e-34:186:97//Z56144  
F-HEMBA1000243//Human DNA sequence from PAC 440021 on chromosome X contains ESTs and STS.//4.1e-67:291:82//Z84481  
F-HEMBA1000244//M.musculus Ank-1 mRNA for erythroid ankyrin.//0.029:316:

59//X69065

F-HEMBA1000251//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence.//0.35:467:60//AC004454

F-HEMBA1000264

F-HEMBA1000280//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//8.9e-20:218:78//AC004825

F-HEMBA1000282//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//4.2e-08:134:77//AC004617

F-HEMBA1000288//345L5.TPB CIT978SKA1 Homo sapiens genomic clone A-345L05, genomic survey sequence.//1.1e-06:152:73//B17459

F-HEMBA1000290//Human ornithine decarboxylase gene, complete cds.//3.2e-11:507:62//M33764

F-HEMBA1000302//CIT-HSP-2169N13.TF CIT-HSP Homo sapiens genomic clone 21 69N13, genomic survey sequence.//5.4e-06:86:88//B90730

F-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//7.9e-11:701:86//AF030131

F-HEMBA1000304//HS\_3006\_A1\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=17 Row=A, genomic survey sequence.//5.2e-40:240:92//AQ118226

F-HEMBA1000307//Mus musculus mRNA for CDV-1R protein.//7.9e-127:815:84//Y10495

F-HEMBA1000327//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.4e-11:87:96//AQ187492

F-HEMBA1000333

F-HEMBA1000338//Homo sapiens chromosome X, PAC 671D9, complete sequence.//4.0e-66:271:84//AF031078

F-HEMBA1000351//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.64:334:60//AC004848

F-HEMBA1000355//Pseudorabies virus serine/threonine kinase (ULPK) gene, partial cds and alkaline nuclease (AN) gene, complete cds.//0.017:313:63 //U25056

F-HEMBA1000356//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.87:198:61//L40178

F-HEMBA1000357//HS\_3194\_A1\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//6.5e-90:436:98//AQ173748

F-HEMBA1000366//HS\_3027\_B2\_G06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=12 Row=N, genomic survey sequence.//0.0074:192:64//AQ128843

F-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//4.2e-106:133:99//AL031587

F-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.6e-22:659:63//AC006116

F-HEMBA1000387//Homo sapiens chromosome 12p13.3 clone RPCI11-264F23, WORKING DRAFT SEQUENCE, 90 unordered pieces.//3.2e-06:136:75//AC006122

F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15, complete sequence.//3.5e-111:284:95//AC004520

F-HEMBA1000392//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//1.8e-39:332:80//AL031984

F-HEMBA1000396//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene, complete sequence.//9.5e-35:364:73//U80460

F-HEMBA1000411//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L 21) from the Roswell Park Cancer Institute, complete sequence.//8.1e-18:424:64//U96409

F-HEMBA1000418//Drosophila melanogaster Oregon-R mitochondrial A+T region

n.//0.0026:564:59//U11584

F-HEMBA1000422//Human DNA from chromosome 19 specific cosmid R30292, genomic sequence, complete sequence.//9.2e-14:232:70//AC003112

F-HEMBA1000428//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//3.8e-37:408:69//AC004554

F-HEMBA1000434//Caenorhabditis elegans cosmid Y48E1B, complete sequence.//0.73:454:57//Z93393

F-HEMBA1000442

F-HEMBA1000456//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-1 1-30J5, genomic survey sequence.//6.3e-06:62:96//B85188

F-HEMBA1000459//Mus musculus hemin-sensitive initiation factor 2 alpha kinase mRNA, complete cds.//6.8e-70:580:79//AF028808

F-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//2.8e-154:746:98//AC004839

F-HEMBA1000464//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.8e-25:397:72//AC006213

F-HEMBA1000469//CIT-HSP-2167P21.TF CIT-HSP Homo sapiens genomic clone 21 67P21, genomic survey sequence.//4.0e-83:406:99//B94160

F-HEMBA1000488//Homo sapiens Chromosome 22q11.2 PAC Clone p\_m11 In BCRL2 -GGT Region, complete sequence.//4.2e-53:312:93//AC004033

F-HEMBA1000490//Campylobacter jejuni groES, groEL genes.//0.59:451:62//Y 13334

F-HEMBA1000491//Murine sarcoma virus (Harvey-strain) H-ras transforming p21 gene.//8.6e-06:338:58//X00740

F-HEMBA1000501//Homo sapiens chromosome 17, clone hRPK.264\_B\_14, complete sequence.//9.4e-41:591:69//AC005884

F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os).//4.0e-07:57:100//D13666

F-HEMBA1000505

F-HEMBA1000508//\*\*\* SEQUENCING IN PROGRESS \*\*\* *Homo sapiens* chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.035:329:61//AC004661

F-HEMBA1000518//*Caenorhabditis elegans* cosmid C17H12.//0.96:425:58//AF045642

F-HEMBA1000519//*Homo sapiens* Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//1.6e-53:300:89//AC004616

F-HEMBA1000520//*Homo sapiens* clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.7e-10:117:86//AC006006

F-HEMBA1000523

F-HEMBA1000531//*Mus musculus* Hsp70-related NST-1 (hsr.1) mRNA, complete cds.//3.9e-35:290:80//U08215

F-HEMBA1000534//*Homo sapiens* chromosome 17, clone hRPK.177\_H\_5, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.7e-36:328:77//AC005973

F-HEMBA1000540//*Arabidopsis thaliana* DNA chromosome 4, BAC clone F7K2 (ESSAI project).//0.057:265:63//AL033545

F-HEMBA1000542//*Rattus norvegicus* mRNA for dipeptidyl peptidase III, complete cds.//1.2e-110:572:88//D89340

F-HEMBA1000545//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//7.5e-130:780:89//Z49237

F-HEMBA1000555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE.//3.2e-175:838:98//AL034555

F-HEMBA1000557//CIT-HSP-2369F15.TF CIT-HSP *Homo sapiens* genomic clone 2369F15, genomic survey sequence.//2.8e-32:315:78//AQ074611

F-HEMBA1000561//*Rattus norvegicus* Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//3.4e-69:665:72//U92564

F-HEMBA1000563//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.59:261:61//AC

005504

F-HEMBA1000568//HS\_3243\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3243 Col=24 Row=B, genomic survey sequence.//3.1e-54:323:91//AQ219628

F-HEMBA1000569//M.musculus mRNA for GPI-anchored protein.//1.4e-19:440:61//X89571

F-HEMBA1000575//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0016:557:57//AC005506

● F-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//1.7e-11:132:79//AF045573

F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.3e-43:228:97//AJ007509

F-HEMBA1000592//Mus musculus clone OST7314, genomic survey sequence.//7.3e-07:68:94//AF046733

F-HEMBA1000594//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//8.7e-71:553:79//Z83822

● F-HEMBA1000604//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 237J2, WORKING DRAFT SEQUENCE.//2.9e-21:158:75//AL021394

● F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.1e-118:561:99//AB007925

F-HEMBA1000622//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//2.2e-28:426:70//AC004382

F-HEMBA1000636//Human CpG island sequence, clone Q28B8.//1.0e-15:274:68//D85773

F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//6.7e-137:639:99//AB014590

F-HEMBA1000655//, complete sequence.//5.1e-83:685:80//AC005815

F-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPases

e activating protein mRNA, complete cds.//1.1e-91:597:84//U35776

F-HEMBA1000662//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//0.019:695:57//AC004907

F-HEMBA1000673//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 229A8, WORKING DRAFT SEQUENCE.//1.5e-48:325:85//Z86090

F-HEMBA1000682//Homo sapiens (subclone 5\_g5 from P1 H25) DNA sequence.//  
7.7e-61:615:74//L43411

F-HEMBA1000686

F-HEMBA1000702

● F-HEMBA1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 geno  
mic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0037:569:57  
//AC005507

F-HEMBA1000719//Streptomyces coelicolor cosmid 1C2.//2.0e-09:483:62//AL0  
31124

F-HEMBA1000722//Toxoplasma gondii chloroplast, complete genome.//0.00058  
:762:57//U87145

F-HEMBA1000726//H.sapiens HLA-DRB1\*15 gene.//9.8e-49:189:89//X88791

F-HEMBA1000727//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 38  
7P22, genomic survey sequence.//0.0054:206:67//B60158

● F-HEMBA1000747

F-HEMBA1000749//Human DNA sequence from clone 522P13 on chromosome 6p21.  
31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3  
(Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs,  
STSs and GSSs, complete sequence.//3.3e-05:124:75//AL024509

F-HEMBA1000752//Human Chromosome X, complete sequence.//5.9e-48:502:75//  
AC004073

F-HEMBA1000769//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//0.011:179:67//AC005043

F-HEMBA1000773//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*

\* from clone Y59A8, WORKING DRAFT SEQUENCE.//0.070:231:63//Z98870

F-HEMBA1000774//*Homo sapiens* PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//6.2e-40:385:75//AC004953

F-HEMBA1000791

F-HEMBA1000817//*Myrmecia pilosula* HI87-135 mitochondrion cytochrome b gene, partial cds.//0.99:244:58//U15678

F-HEMBA1000822//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island.//0.033:294:62//Z81370

F-HEMBA1000827//*Borrelia burgdorferi* (section 50 of 70) of the complete genome.//9.7e-05:463:58//AE001164

F-HEMBA1000843//*Homo sapiens* DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//3.0e-153:732:98//AL022394

F-HEMBA1000851//*Rattus norvegicus* glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//1.6e-31:386:72//AF059273

F-HEMBA1000852//*Homo sapiens* Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//8.5e-115:455:98//AC005295

F-HEMBA1000867

F-HEMBA1000869//Human DNA sequence from cosmid J138017, between markers DDX6791 and DDX8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element.//6.6e-41:424:75//Z72519

F-HEMBA1000870//*Gnampydon pumilio* cytochrome oxidase II gene, partial cds; and tRNA-Asp, tRNA-His, and tRNA-Lys genes, complete sequence, mitoc

hondrial genes for mitochondrial products.//0.0049:211:66//AF034598

F-HEMBA1000872//CIT-HSP-2355D20.TF CIT-HSP Homo sapiens genomic clone 23  
55D20, genomic survey sequence.//3.7e-33:180:98//AQ059583

F-HEMBA1000876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 473B4, WORKING DRAFT SEQUENCE.//5.6e-37:262:72//Z83826

F-HEMBA1000908//Triticum aestivum low-affinity cation transporter (LCT1)  
mRNA, complete cds://1.0:304:59//AF015523

F-HEMBA1000910//M.musculus necdin mRNA, complete cds.//6.1e-08:256:61//M  
80840

● F-HEMBA1000918//Tetrahymena thermophila micronuclear developmentally eli  
minated sequence region.//0.13:232:63//U88158

F-HEMBA1000919//Gallus domesticus filamin mRNA, complete cds.//1.0:213:6  
5//U00147

F-HEMBA1000934//CIT-HSP-2053H24.TR CIT-HSP Homo sapiens genomic clone 20  
53H24, genomic survey sequence.//5.5e-11:275:64//B69224

F-HEMBA1000942//Homo sapiens clone DJ0754G14, WORKING DRAFT SEQUENCE, 15  
unordered pieces.//9.7e-05:78:83//AC004878

F-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complet  
e sequence.//5.8e-140:661:99//AC005324

● F-HEMBA1000946

F-HEMBA1000960//Homo sapiens clone DJ1111F22, WORKING DRAFT SEQUENCE, 12  
unordered pieces.//8.3e-16:181:75//AC004967

F-HEMBA1000968//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 69M21, WORKING DRAFT SEQUENCE.//4.4e-117:398:86//AL031735

F-HEMBA1000971//H.sapiens CpG island DNA genomic Mse1 fragment, clone 18  
2f4, forward read cpg182f4.ft1a.//1.5e-20:126:96//Z57528

F-HEMBA1000972//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of  
hepatocellular colorectal and non-small cell lung cancer , segment 1/11.  
//0.34:642:59//AB020858

F-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//5.1e-1  
83:865:98//AC004817

F-HEMBA1000975//Orf virus homologue of retroviral pseudoprotease gene, c  
omplete cds.//0.00065:391:62//M30023

F-HEMBA1000985//Human DNA sequence from clone 272E8 on chromosome Xp22.1  
3-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein  
gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequenc  
e.//3.4e-05:243:65//Z93929

F-HEMBA1000986//Homo sapiens DNA from chromosome 19-cosmid R31491, genom  
ic sequence.//6.6e-06:508:61//AD000813

F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds.//1.2e-22:193:84  
//D84064

F-HEMBA1001007

F-HEMBA1001008//Human DNA sequence from clone 391022 on chromosome 6p21.  
2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, c  
omplete sequence.//7.8e-46:532:73//AL031577

F-HEMBA1001009//Human mRNA for IgM heavy chain complete sequence.//0.97:  
369:59//X17115

F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//4  
.4e-139:661:98//AB007937

F-HEMBA1001019//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//1.6  
e-16:521:64//AC006213

F-HEMBA1001020//Homo sapiens chromosome 17, clone hRPK.178\_C\_3, complete  
sequence.//3.8e-50:367:72//AC005702

F-HEMBA1001022

F-HEMBA1001024//Homo sapiens T-cell receptor alpha delta locus from base  
s 1 to 250529 (section 1 of 5) of the Complete Nucleotide Sequence.//5.0  
e-23:378:69//AE000658

F-HEMBA1001026//Homo sapiens DNA sequence from PAC 435D1 on chromosome X

q25. Contains ESTs and STS.//7.6e-19:867:60//Z86064

F-HEMBA1001043//HS\_2219\_B1\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=19 Row=B, genomic survey sequence.//3.0e-15:124:88//AQ301521

F-HEMBA1001051//Human Chromosome X clone bWxD342, complete sequence.//4.8e-79:308:84//AC004072

F-HEMBA1001052//Homo sapiens chromosome 17, clone hRPK.146\_P\_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.53:384:61//AC005341

F-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 10.//2.8e-26:397:71//U06084

F-HEMBA1001060//Homo sapiens chromosome 17, clone hRPK.855\_D\_21, complete sequence.//0.98:280:62//AC006079

F-HEMBA1001071//Human mRNA for pro alpha 1 (III) collagen C-terminal pro peptide.//1.1e-31:181:96//X01742

F-HEMBA1001077//nuclear protein TIF1 [mice, mRNA, 3951 nt].//3.6e-13:338:65//S78219

F-HEMBA1001080//Streptomyces coelicolor cosmid 1A9.//0.00012:364:63//AL034446

F-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.5e-134:476:96//AC004586

F-HEMBA1001088//Sequence 1 from patent US 5552529.//2.2e-71:303:78//I25863

F-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//8.9e-119:609:96//AC005105

F-HEMBA1001099

F-HEMBA1001109//Homo sapiens BAC clone RG318M05 from 7q22-q31.1, complete sequence.//2.4e-58:347:87//AC005250

F-HEMBA1001121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 90G24, WORKING DRAFT SEQUENCE.//3.4e-21:226:65//AL008723

F-HEMBA1001122//*Plasmodium falciparum* chromosome 2, section 20 of 73 of the complete sequence.//9.2e-07:732:57//AE001383

F-HEMBA1001123//*Homo sapiens* full length insert cDNA clone ZD38E12.//1.1e-11:231:68//AF086247

F-HEMBA1001133//*Homo sapiens* clone DJ0856024, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.011:163:69//AC004909

F-HEMBA1001137//*Homo sapiens* mRNA for KIAA0798 protein, complete cds.//6.9e-72:527:77//AB018341

F-HEMBA1001140//*Homo sapiens* clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.3e-120:578:98//AC005077

F-HEMBA1001172//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.010:520:59//AC005507

F-HEMBA1001174//*R. norvegicus* (Sprague Dawley) ARL5 mRNA for ARF-like protein 5.//1.0e-59:565:73//X78604

F-HEMBA1001197//*Homo sapiens* clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0037:151:70//AC004815

F-HEMBA1001208//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//7.4e-35:195:81//AC002410

F-HEMBA1001213//*Homo sapiens* clone DJ0892G19, complete sequence.//1.9e-171:826:98//AC004917

F-HEMBA1001226//*Homo sapiens* clone DJ0850I01, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.00010:557:57//AC006009

F-HEMBA1001235//*Homo sapiens* chromosome 17, clone hRPK.601\_N\_13, complete sequence.//0.0086:372:58//AC005389

F-HEMBA1001247//*H. sapiens* CpG island DNA genomic Mse1 fragment, clone 11b11, reverse read cpg11b11.rt1a.//2.0e-24:154:93//Z64441

F-HEMBA1001257//*Homo sapiens* alpha-methylacyl-CoA racemase mRNA, complete

e cds.//1.9e-88:659:81//AF047020

F-HEMBA1001265//Human 18S ribosomal RNA.//1.0e-32:180:97//X03205

F-HEMBA1001281

F-HEMBA1001286//B.taurus mRNA for RF-36-DNA-binding protein.//7.7e-26:23  
6:81//X15543

F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, c  
omplete sequence.//5.5e-28:530:64//AC004131

F-HEMBA1001294//Yeast mitochondrial aap1 gene for ATPase subunit 8.//2.8  
e-15:722:60//X00960

F-HEMBA1001299//Human DNA sequence from clone 422G23 on chromosome 6q24  
Contains EST, STS, GSS, CpG island, complete sequence.//4.2e-24:288:76//  
AL031003

F-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypep  
tide derived from stromal cell.//7.2e-121:439:96//E12260

F-HEMBA1001303//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic  
sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.011:637:56//AC  
005505

F-HEMBA1001310//HS\_3252\_B2\_B12\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3252 Col=24 Row=D, genomic survey  
sequence.//1.2e-16:166:82//AQ217054

F-HEMBA1001319//CIT-HSP-2034J6.TF CIT-HSP Homo sapiens genomic clone 203  
4J6, genomic survey sequence.//0.33:256:59//B79408

F-HEMBA1001323//Homo sapiens proto-oncogene (Wnt-5a) mRNA, complete cds.  
//7.8e-30:165:99//L20861

F-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6  
. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a  
beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE ps  
eudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudo  
gene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences)

and a CA repeat polymorphism, complete sequence.//5.4e-19:347:68//AL021

368

F-HEMBA1001327//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 23  
54E10, genomic survey sequence.//0.012:152:65//AQ075713

F-HEMBA1001330//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from contig 3-103, complete sequence.//0.0037:254:62//AL010208

F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33)  
mRNA, complete cds.//1.1e-103:516:97//AF057358

F-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete  
sequence.//1.7e-150:706:99//AC006241

F-HEMBA1001375//Streptomyces coelicolor cosmid 1E6.//1.0:375:59//AL03350  
5

F-HEMBA1001377//HS\_3020\_B1\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3020 Col=23 Row=H, genomic survey sequence.//0.00022:63:77//AQ105297

F-HEMBA1001383//Plasmodium falciparum chromosome 2, section 68 of 73 of  
the complete sequence.//0.00035:317:60//AE001431

F-HEMBA1001387//HS\_3039\_B1\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//5.0e-90:437:98//AQ155035

F-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15  
unordered pieces.//4.2e-47:159:89//AC005073

F-HEMBA1001391//Human DNA sequence from clone 409010 on chromosome 20q12  
Contains CA repeat, GSS, STS, complete sequence.//2.0e-06:495:60//AL031

256

F-HEMBA1001398//H.sapiens CpG island DNA genomic Mse1 fragment, clone 70  
d11, forward read cpg70d11.ft1b.//0.018:46:97//Z62591

F-HEMBA1001405//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.//2.3e-74:623:71//AL034380

F-HEMBA1001407//*Mus musculus domesticus* Torino (Sry) gene, complete cds.

//0.36:363:57//U03645

F-HEMBA1001411//*Homo sapiens* genomic DNA, 21q region, clone: S39BG29, genomic survey sequence.//8.4e-12:516:60//AG001050

F-HEMBA1001413

F-HEMBA1001415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING DRAFT SEQUENCE.//0.98:177:64//AL031732

F-HEMBA1001432//*Homo sapiens* clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.0e-177:859:97//AC006146

F-HEMBA1001433//*Homo sapiens* clone DJ0892G19, complete sequence.//2.0e-3 5:376:64//AC004917

F-HEMBA1001435//*Homo sapiens* chromosome 17, clone hRPK.63\_A\_1, complete sequence.//1.2e-74:284:84//AC005670

F-HEMBA1001442//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-66, complete sequence.//0.056:194:63//AL010138

F-HEMBA1001446//*Homo sapiens* chromosome 4 clone B150J4 map 4q25, complete sequence.//0.96:328:61//AC004047

F-HEMBA1001450

F-HEMBA1001454//Human DNA sequence from clone 598A24 on chromosome Xp11.

1-11.23 Contains zinc finger X-linked proteins ZXDA, ZXDB. ESTs and STS, complete sequence.//2.0e-47:468:73//AL031115

F-HEMBA1001455//CIT978SK-32J2.TV CIT978SK *Homo sapiens* genomic clone 32J 2, genomic survey sequence.//1.5e-05:223:65//B78859

F-HEMBA1001463//cSRL-69d1-u cSRL flow sorted Chromosome 11 specific cosm id *Homo sapiens* genomic clone cSRL-69d1, genomic survey sequence.//5.1e-66:564:77//B05652

F-HEMBA1001476//*Homo sapiens* mRNA for KIAA0572 protein, partial cds.//1.9e-102:489:99//AB011144

F-HEMBA1001478//HS\_2228\_A2\_B03\_MF CIT Approved Human Genomic Sperm Libra

ry D *Homo sapiens* genomic clone Plate=2228 Col=6 Row=C, genomic survey sequence.//4.5e-40:275:88//AQ032041

F-HEMBA1001497//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//7.7e-47:311:85//AL031133

F-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//2.0e-130:699:93//U89337

F-HEMBA1001515//*Homo sapiens* chromosome 19, cosmid F24866, complete sequence.//4.1e-114:711:85//AC005794

F-HEMBA1001517//*Homo sapiens* BAC clone RG459N13 from 7p15, complete sequence.//5.7e-162:769:98//AC004549

F-HEMBA1001522//*Caenorhabditis elegans* cosmid ZK328.//8.6e-17:498:61//U50193

F-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands.//0.31:120:69//Z98258

F-HEMBA1001533

F-HEMBA1001557//*Chionoecetes opilio* (clone COP41) DNA microsatellite repeat regions.//7.0e-25:303:72//L49136

F-HEMBA1001566//*Homo sapiens* DNA sequence from PAC 127D3 on chromosome 1 q23-25. Contains FM02 and FM03 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//7.2e-18:805:60//AL02102

F-HEMBA1001569//*Homo sapiens* mRNA for vesicle associated membrane protein 2 (VAMP2).//1.1e-64:338:95//AJ225044

F-HEMBA1001570//*Homo sapiens* PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.1e-148:698:99//AC004453

F-HEMBA1001579//*Homo sapiens* mRNA for NS1-binding protein (NS1-BP).//2.2e-173:678:99//AJ012449

F-HEMBA1001581//*Homo sapiens* clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.30:484:59//AC004980

F-HEMBA1001585

F-HEMBA1001589//Human BAC clone RG317G18 from 7q31, complete sequence.//0.98:197:63//AC002432

F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds.//8.2e-109:855:78//D50918

F-HEMBA1001608//RPCI11-72E2.TJ RPCI11 *Homo sapiens* genomic clone R-72E2, genomic survey sequence.//3.8e-05:235:64//AQ267131

F-HEMBA1001620//*Oryza sativa* RIN01 mRNA for myo-inositol phosphate synthase, complete cds.//3.8e-40:719:64//AB012107

F-HEMBA1001635//HS\_3208\_A1\_D07\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3208 Col=13 Row=G, genomic survey sequence.//1.4e-15:120:90//AQ176944

F-HEMBA1001636//*Homo sapiens* 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.15:221:64//AC004216

F-HEMBA1001640//HS\_3253\_B2\_D03\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3253 Col=6 Row=H, genomic survey sequence.//9.1e-52:278:95//AQ216058

F-HEMBA1001647//*H.sapiens* gene for plectin.//0.00052:629:61//Z54367

F-HEMBA1001651//*Salmo* *salar* DNA for a cryptic repeat.//7.9e-08:270:64//AJ012206

F-HEMBA1001655//*Homo sapiens* chromosome 5, BAC clone 194j18 (LBNL H158),  
complete sequence.//5.9e-164:802:97//AC005368

F-HEMBA1001658//*M. musculus* COL3A1 gene for collagen alpha-I.//2.4e-30:74  
2:62//X52046

F-HEMBA1001661//*Homo sapiens* chromosome 5p, BAC clone 50g21 (LBNL H154),  
complete sequence.//2.2e-144:682:99//AC005740

F-HEMBA1001672//*Homo sapiens* methyl-CpG binding protein MBD3 (MBD3) mRNA  
, complete cds.//6.1e-152:725:98//AF072247

F-HEMBA1001675//RPCI11-54F8.TV RPCI11 *Homo sapiens* genomic clone R-54F8,  
genomic survey sequence.//5.3e-75:341:85//AQ082126

F-HEMBA1001678//*Homo sapiens* Xp22 PAC RPCI1-167A22 (from Roswell Park Ca  
ncer Center) complete sequence.//8.4e-54:551:74//AC002349

F-HEMBA1001681

F-HEMBA1001702//*Plasmodium falciparum* chromosome 2, section 35 of 73 of  
the complete sequence.//0.94:676:54//AE001398

F-HEMBA1001709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 702J19, WORKING DRAFT SEQUENCE.//0.74:659:58//AL033531

F-HEMBA1001711//*Lysiphlebus melandriicola* NADH dehydrogenase 1 gene, mit  
ochondrial gene encoding mitochondrial protein, partial cds.//3.0e-07:41  
3:60//AF069178

F-HEMBA1001712//*Homo sapiens* BAC clone RG041H04 from 7q21-q22, complete  
sequence.//0.091:315:61//AC004519

F-HEMBA1001714//*Rattus norvegicus* mitochondrial ATPase inhibitor gene, c  
omplete cds.//1.6e-28:218:75//U12250

F-HEMBA1001718//HS\_3056\_A2\_H08\_MF CIT Approved Human Genomic Sperm Libra  
ry D *Homo sapiens* genomic clone Plate=3056 Col=16 Row=0, genomic survey  
sequence.//2.0e-79:383:99//AQ106367

F-HEMBA1001723//HS\_2188\_A2\_D02\_MF CIT Approved Human Genomic Sperm Libra  
ry D *Homo sapiens* genomic clone Plate=2188 Col=4 Row=G, genomic survey s

quence.//3.8e-28:174:94//AQ116793

F-HEMBA1001731//HS\_3021\_A1\_A11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=21 Row=A, genomic survey sequence.//2.5e-11:420:62//AQ154658

F-HEMBA1001734//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.00060:392:60//AC004617

F-HEMBA1001744//HS\_3194\_A1\_D05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//5.8e-29:163:97//AQ252295

F-HEMBA1001745//Homo sapiens chromosome 9q34, clone 280C11, complete sequence.//0.66:627:59//AC002102

F-HEMBA1001746//HS\_2163\_B1\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=7 Row=L, genomic survey sequence.//1.4e-16:238:70//AQ085995

F-HEMBA1001761//Genomic sequence from Mouse 9, complete sequence.//3.5e-52:198:86//AC002109

F-HEMBA1001781

F-HEMBA1001784//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-13:296:65//AC002099

F-HEMBA1001791//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//0.18:534:59//AF038458

F-HEMBA1001800//CIT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//2.2e-40:335:80//AQ009222

F-HEMBA1001803//M.musculus (Balb/C) P/L01 mRNA.//1.7e-25:286:74//Z31360

F-HEMBA1001804//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-58:358:89//M21977

F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//7.8e-174:809:98//AB007969

F-HEMBA1001809//Bovine herpesvirus 1 complete genome.//9.0e-09:639:57//A

J004801

F-HEMBA1001815

F-HEMBA1001819//HS\_3079\_B1\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=J, genomic survey sequence.//1.4e-79:396:97//AQ186616

F-HEMBA1001820//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//0.00026:436:60//AC005013

F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds.//1.2e-40:510:65//AF064243

F-HEMBA1001824//Homo sapiens expanded SCA7 CAG repeat.//6.1e-20:344:68//AF020275

F-HEMBA1001835//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.0094:553:58//AC005161

F-HEMBA1001844//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//1.2e-22:316:70//AC005867

F-HEMBA1001847//M.musculus Zfp-29 gene for zinc finger protein.//5.3e-27:397:69//X55126

F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//8.8e-184:865:98//AB014517

F-HEMBA1001864//Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence.//0.38:337:62//AC005395

F-HEMBA1001866//Caenorhabditis elegans cosmid F48E3.//1.4e-10:224:63//U28735

F-HEMBA1001869//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//6.7e-98:288:91//AC005065

F-HEMBA1001888//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//4.9e-114:476:84//AC003693

F-HEMBA1001896//Bos taurus pyruvate dehydrogenase phosphatase regulatory

subunit precursor, mRNA, complete cds.//2.2e-137:839:86//AF026954  
F-HEMBA1001910//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//0.90:221:63//AC003065  
F-HEMBA1001912//HS\_2237\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//9.7e-76:364:100//AQ033732  
F-HEMBA1001913//Leishmania major chromosome 3 clone L4625 strain Friedlin, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.00063:219:65//AC005766  
F-HEMBA1001915//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer , segment 5/10.//0.00011:366:63//AB020873  
F-HEMBA1001918//Pneumocystis carinii gene for major surface glycoprotein MSG105, exon1-2, complete cds.//0.00024:562:58//D82031  
F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.1e-184:855:99//AF000145  
F-HEMBA1001939//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.1e-42:380:80//AL022310  
F-HEMBA1001940//Homo sapiens clone DJ1093I16, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-175:861:97//AC005629  
F-HEMBA1001942//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//0.097:107:71//AC006057  
F-HEMBA1001945//Drosophila F family transposable element F12 3' region.//0.94:140:65//X01934  
F-HEMBA1001950//H.sapiens CpG island DNA genomic Mse1 fragment, clone 15 b5, forward read cpg15b5.ft1q.//1.4e-27:168:95//Z54728  
F-HEMBA1001960//Locusta migratoria mRNA for nAChR alpha1 subunit.//0.010

:108:71//AJ000390

F-HEMBA1001962//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.7e-05:494:60//AC005507

F-HEMBA1001964

F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isoform of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//9.6e-122:373:99//AL031178

F-HEMBA1001979//HS\_3067\_B1\_A06\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3067 Col=11 Row=B, genomic survey sequence.//0.43:193:64//AQ143506

F-HEMBA1001987//*Plasmodium falciparum* MAL3P6, complete sequence.//1.0:42:56//Z98551

F-HEMBA1001991//HS\_2237\_A2\_G09\_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2237 Col=18 Row=M, genomic survey sequence.//4.3e-05:240:64//AQ067283

F-HEMBA1002003//protein phosphatase 2C isoform [rats, liver, mRNA, 1950 nt].//2.7e-33:364:74//S90449

F-HEMBA1002008//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00032:214:68//AC005948

F-HEMBA1002018

F-HEMBA1002022//Human p37NB mRNA, complete cds.//0.014:58:96//U32907

F-HEMBA1002035//Mouse transcriptional control element.//7.8e-07:200:69//M17284

F-HEMBA1002039//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//0.31:497:58//AL031053

F-HEMBA1002049//*Homo sapiens* chromosome 5, BAC clone 282B7 (LBNL H192),  
complete sequence.//4.5e-42:532:63//AC005216

F-HEMBA1002084//*Homo sapiens* chromosome 19 cosmid F15386, genomic sequence,  
complete sequence.//0.81:435:59//AF025422

F-HEMBA1002092//*Mus musculus* Olf-1/EBF-like-3 transcription factor (O/E-  
3) mRNA, complete cds.//7.2e-130:769:87//U92703

F-HEMBA1002100//*Homo sapiens* PAC clone DJ0991G20, complete sequence.//1.  
3e-47:124:96//AC004943

F-HEMBA1002102//*Xenopus laevis* mRNA for xSox7 protein, complete cds.//2.  
7e-13:132:71//D83649

F-HEMBA1002113//*F. rubripes* GSS sequence, clone 063K10bB4, genomic survey  
sequence.//0.029:142:66//Z88840

F-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1  
.3e-14:515:62//AC000378

F-HEMBA1002125//*Homo sapiens* calcium-activated potassium channel (KCNN3)  
mRNA, complete cds.//0.98:222:61//AF031815

F-HEMBA1002139//*Caenorhabditis elegans* cosmid F55C9, complete sequence.//  
/0.0081:371:60//Z81549

F-HEMBA1002144//*Saccharomyces cerevisiae* mitochondrial transfer RNA-Met  
(tRNA-Met) gene, oxil gene, and ORF1.//4.9e-06:341:61//L36888

F-HEMBA1002150//*Homo sapiens* mRNA for KIAA0720 protein, partial cds.//0.  
00017:353:62//AB018263

F-HEMBA1002151

F-HEMBA1002153//CITBI-E1-2519I20.TR CITBI-E1 *Homo sapiens* genomic clone  
2519I20, genomic survey sequence.//8.5e-61:334:94//AQ277613

F-HEMBA1002160//*Homo sapiens* clone DJ1189D06, complete sequence.//8.5e-4  
4:385:77//AC005232

F-HEMBA1002161//*Coturnix coturnix* slow myosin heavy chain 2 (qmyhc2) mRNA  
, partial cds.//2.1e-59:571:74//AF006829

F-HEMBA1002162//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//5.3e-53:698:67//AC006210

F-HEMBA1002166//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-50:319:78//AL008712

F-HEMBA1002177//Homo sapiens BAC clone RG293F11 from 7q21-7q22, complete sequence.//2.5e-18:150:88//AC000066

F-HEMBA1002185//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00066:466:59//AC004825

F-HEMBA1002189//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-23:176:77//AC005015

F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds.//1.0:382:59//AB014589

F-HEMBA1002199//Homo sapiens chromosome 4 clone B55B24 map 4q25, complete sequence.//1.8e-20:368:66//AC005150

F-HEMBA1002204//HS\_2055\_A1\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=17 Row=0, genomic survey sequence.//1.2e-06:178:65//AQ235350

F-HEMBA1002212//S.cerevisiae chromosome IV reading frame ORF YDL101c.//0.035:345:60//Z74149

F-HEMBA1002215//M.musculus mRNA for testin.//4.6e-80:504:87//X78989

F-HEMBA1002226//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-63:336:74//AC003035

F-HEMBA1002229//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//2.6e-39:311:81//AC006044

F-HEMBA1002237//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//1.6e-12:397:64//AC004861

F-HEMBA1002241

F-HEMBA1002253

F-HEMBA1002257//*Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds.*//3.5e-151:731:97//AF061936

F-HEMBA1002265//*Human DNA sequence from cosmid N28H9 on chromosome 22q11.2-qter contains ESTs, STS and endogenous retrovirus.*//1.3e-09:313:62//Z  
71183

F-HEMBA1002267

F-HEMBA1002270//*Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.*//0.069:495:58//AC006210

F-HEMBA1002321//*Homo sapiens PAC clone DJ0991023, complete sequence.*//0.019:564:58//AC004944

F-HEMBA1002328//*CIT-HSP-2387N15.TF.1 CIT-HSP Homo sapiens genomic clone 2387N15, genomic survey sequence.*//1.8e-71:346:99//AQ240836

F-HEMBA1002337//*Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MYN8, complete sequence.*//0.84:547:57//AB020754

F-HEMBA1002341//*Homo sapiens mRNA for KIAA0771 protein, partial cds.*//2.4e-185:872:98//AB018314

F-HEMBA1002348//*CIT-HSP-2372K24.TR CIT-HSP Homo sapiens genomic clone 2372K24, genomic survey sequence.*//9.1e-33:230:75//AQ110676

F-HEMBA1002349//*Plasmodium falciparum histidine-rich protein II (HRP II) gene, complete cds.*//9.4e-06:504:57//U69551

F-HEMBA1002363//*Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.*//7.3e-188:872:99//AF092563

F-HEMBA1002381//*Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 11/11*//2.1e-20:262:72//AB020868

F-HEMBA1002389//*D. discoideum spore coat 60 (sp60) gene, 5' flank.*//0.010:95:73//M34546

F-HEMBA1002417//*Canis familiaris ZO-3 (zo-3) mRNA, complete cds.*//6.2e-1

20:767:85//AF023617

F-HEMBA1002419//HS-1047-A1-F01-MF.abi CIT Human Genomic Sperm Library C  
Homo sapiens genomic clone Plate=CT 830 Col=1 Row=K, genomic survey sequence.//7.6e-06:111:76//B38165

F-HEMBA1002430//HS\_3137\_B2\_F10\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3137 Col=20 Row=L, genomic survey sequence.//1.6e-56:367:88//AQ148697

F-HEMBA1002439//Dictyostelium discoideum actin 8 gene, 3' UTR.//0.67:129  
:64//M25216

● F-HEMBA1002458//Mus musculus REX-3 mRNA, complete cds.//1.1e-30:274:72//  
AF051347

F-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-1  
73:822:98//AC005378

F-HEMBA1002462//Sequence 41 from patent US 5708157.//9.8e-51:519:73//I80  
067

F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds.//4.0e-108:603  
:92//D50912

F-HEMBA1002475//Streptomyces coelicolor cosmid 2H4.//0.0068:626:57//AL03  
1514

● F-HEMBA1002477//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//1.5e-40:349:78//AC005034

F-HEMBA1002486

F-HEMBA1002495//HS\_3218\_B1\_A12\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3218 Col=23 Row=B, genomic survey sequence.//1.0:179:67//AQ181410

F-HEMBA1002498//Homo sapiens full length insert cDNA clone ZD76B01.//1.4  
e-129:619:98//AF086404

F-HEMBA1002503//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6  
unordered pieces.//1.9e-24:306:68//AC004873

F-HEMBA1002508//*Homo sapiens* chromosome 19, cosmid R33516, complete sequence.//2.9e-76:464:83//AC004799

F-HEMBA1002513//*Homo sapiens* mRNA for histone deacetylase-like protein (JM21).//2.8e-157:738:98//AJ011972

F-HEMBA1002515//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 407F11, WORKING DRAFT SEQUENCE.//2.6e-07:307:64//AL022329

F-HEMBA1002538//HS\_2185\_B2\_B04\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2185 Col=8 Row=D, genomic survey sequence.//4.7e-37:339:78//AQ298315

● F-HEMBA1002542//HS\_3197\_B2\_B10\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//3.2e-70:372:95//AQ188792

F-HEMBA1002547//*Homo sapiens* agrin precursor mRNA, partial cds.//3.5e-13 7:655:98//AF016903

F-HEMBA1002552//Human Hep27 protein mRNA, complete cds.//8.8e-07:173:68//U31875

F-HEMBA1002555//\*\*\* SEQUENCING IN PROGRESS \*\*\* *Homo sapiens* chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.2e-15:628:60//AC004670

● F-HEMBA1002558//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics), PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-41:353:76//AC002366

F-HEMBA1002561//*Homo sapiens* chromosome 17, clone HRPC29G21, complete sequence.//1.1e-39:538:66//AC003687

F-HEMBA1002569//*Homo sapiens* protein associated with Myc mRNA, complete cds.//1.3e-140:457:99//AF075587

F-HEMBA1002583//CIT-HSP-2321D3.TR CIT-HSP *Homo sapiens* genomic clone 232 1D3, genomic survey sequence.//5.1e-79:385:99//AQ038102

F-HEMBA1002590//*Homo sapiens* chromosome 17, clone hRPK.167\_N\_20, complet

e sequence.//1.9e-35:430:70//AC005940

F-HEMBA1002592//Human genomic DNA sequence from clone 30801 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//4.4e-19:303:71//Z93403

F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//4.4e-175:820:99//AB011169

F-HEMBA1002621//Homo sapiens PAC clone DJ0650P09 from 7q21, complete sequence.//0.14:353:58//AC004413

F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//2.9e-187:632:97//AB018351

F-HEMBA1002628//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-05:792:58//AC004153

F-HEMBA1002629//Streptomyces coelicolor cosmid 1A9.//8.4e-08:576:58//AL034446

F-HEMBA1002645//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//5.6e-47:222:86//AL031118

F-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//3.8e-182:859:99//AC004839

F-HEMBA1002659//Z. mobilis alcohol dehydrogenase I (adhA) gene, complete cds.//0.97:144:66//M32100

F-HEMBA1002661//Homo sapiens PAC clone DJ0698G21 from 7p21-p22, complete sequence.//1.3e-116:774:84//AC004535

F-HEMBA1002666

F-HEMBA1002678//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORKING DRAFT SEQUENCE.//5.7e-156:750:98//AL034421

F-HEMBA1002679//nbxb0002cC12r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002F23r, genomic survey sequence.//4.3e-09:517:58//AQ051621

F-HEMBA1002688//Herpes simplex virus type 2 (strain HG52), complete geno

me.//8.3e-20:651:61//Z86099

F-HEMBA1002696//Mus musculus proteasome regulator PA28 beta subunit gene  
, complete cds.//7.6e-62:306:81//AF060195

F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds.//1  
.9e-10:327:62//AB007924

F-HEMBA1002712

F-HEMBA1002716//HS\_3064\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=19 Row=E, genomic survey sequence.//8.4e-97:491:96//AQ142980

F-HEMBA1002728//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170),  
complete sequence.//6.1e-21:217:77//AC004782

F-HEMBA1002730//Human platelet glycoprotein IIIa (GPIIIa) gene, exon 1.//  
/0.57:125:67//M57481

F-HEMBA1002742//RPCI11-39J10.TP RPCI-11 Homo sapiens genomic clone RPCI-  
11-39J10, genomic survey sequence.//1.1e-86:414:99//AQ029102

F-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete se-  
quence.//7.1e-70:303:82//AC003694

F-HEMBA1002748//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c-  
lone 410I8, WORKING DRAFT SEQUENCE.//0.096:212:62//AL031732

F-HEMBA1002750//Homo sapiens chromosome 5, PAC clone 170m10 (LBNL H89),  
complete sequence.//6.7e-40:232:70//AC004622

F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.  
0e-177:834:98//AB011126

F-HEMBA1002770//cDNA encoding novel rat protein TIP120 which is formed o-  
f complex with TBP (TATA binding protein).//1.3e-140:840:88//E12829

F-HEMBA1002777//F.rubripes GSS sequence, clone 189C06dB12, genomic surve-  
y sequence.//1.1e-28:263:77//AL007965

F-HEMBA1002779//CIT-HSP-2333I1.TF CIT-HSP Homo sapiens genomic clone 233  
3I1, genomic survey sequence.//1.8e-32:180:98//AQ036891

F-HEMBA1002780//*Homo sapiens* PAC clone DJ0244J05 from 5q31, complete sequence.//7.0e-06:199:67//AC004592

F-HEMBA1002794//*H.sapiens* mRNA for protein kinase C mu.//0.00015:244:67//X75756

F-HEMBA1002801//*Plasmodium falciparum* MAL3P2, complete sequence.//0.0010:534:57//AL034558

F-HEMBA1002810//*Homo sapiens* formin binding protein 21 mRNA, complete cds.//1.1e-167:820:97//AF071185

F-HEMBA1002816//*Homo sapiens* clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-113:254:90//AC005043

F-HEMBA1002818//*Cricetulus griseus* H411 precursor (H411) mRNA, complete cds.//1.2e-122:760:86//AF046870

F-HEMBA1002826//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.0055:235:65//AL022153

F-HEMBA1002833//*Homo sapiens* chromosome 17, clone hRPC.117\_B\_12, complete sequence.//1.4e-170:744:99//AC004707

F-HEMBA1002850//*Ephedrus persicae* NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//1.3e-05:334:59//AF069186

F-HEMBA1002863//CIT-HSP-2323A16.TF CIT-HSP *Homo sapiens* genomic clone 2323A16, genomic survey sequence.//2.9e-140:750:93//AQ028419

F-HEMBA1002876//HS\_2270\_B1\_H03\_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2270 Col=5 Row=P, genomic survey sequence.//0.44:163:64//AQ164031

F-HEMBA1002886

F-HEMBA1002896//*Homo sapiens* chromosome 5, P1 clone 793C5 (LBNL H58), complete sequence.//0.00015:277:61//AC005195

F-HEMBA1002921

F-HEMBA1002924//CIT-HSP-2171H4.TR CIT-HSP *Homo sapiens* genomic clone 217

1H4, genomic survey sequence.//0.0016:175:66//B89715

F-HEMBA1002934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c lone 862K6, WORKING DRAFT SEQUENCE.//1.2e-169:797:98//AL031681

F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//4. 9e-173:803:99//AB011148

F-HEMBA1002937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c lone 702J19, WORKING DRAFT SEQUENCE.//1.2e-163:411:99//AL033531

F-HEMBA1002939//RPCI11-74014.TJ RPCI11 Homo sapiens genomic clone R-74014, genomic survey sequence.//1.7e-41:215:99//AQ266676

F-HEMBA1002944//RPCI11-55C2.TV RPCI11 Homo sapiens genomic clone R-55C2, genomic survey sequence.//1.7e-37:375:74//AQ082240

F-HEMBA1002951//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//0.00074:683:58//AC005578

F-HEMBA1002954//RPCI11-79F7.TV RPCI11 Homo sapiens genomic clone R-79F7, genomic survey sequence.//6.1e-24:250:78//AQ284146

F-HEMBA1002968//HS\_2262\_B2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=8 Row=N, genomic survey sequence.//0.99:270:60//AQ217059

F-HEMBA1002970//RPCI11-5L24.TV RPCI-11 Homo sapiens genomic clone RPCI-11-5L24, genomic survey sequence.//1.4e-10:189:71//B49289

F-HEMBA1002971//CIT-HSP-2363L16.TF CIT-HSP Homo sapiens genomic clone 2363L16, genomic survey sequence.//4.3e-21:181:80//AQ080538

F-HEMBA1002973//Rattus norvegicus Wistar 3',5' -cyclic AMP phosphodiester ase (PDE4-10) gene, exon 10.//2.5e-40:257:89//U01290

F-HEMBA1002997//CIT-HSP-2387H15.TF.1 CIT-HSP Homo sapiens genomic clone 2387H15, genomic survey sequence.//9.5e-17:128:92//AQ240797

F-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.1e-62:713:73//U20286

F-HEMBA1003021//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3

unordered pieces.//7.5e-50:331:85//AC005484

F-HEMBA1003033//Drosophila melanogaster, chromosome 3L, region 62A10-62B  
5, P1 clones DS02777, DS03222, DS02345, and DS04808, complete sequence.//  
/2.6e-20:357:66//AC005557

F-HEMBA1003034//Human DNA sequence from 4PTEL, Huntington's Disease Regi  
on, chromosome 4p16.3.//4.5e-60:415:73//Z95704

F-HEMBA1003035//Homo sapiens chromosome Y, clone 264,M,20, complete sequ  
ence.//2.3e-05:591:57//AC004617

F-HEMBA1003037//RPCI11-88F2.TJ RPCI11 Homo sapiens genomic clone R-88F2,  
genomic survey sequence.//0.68:230:60//AQ286677

F-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, comp  
lete sequence.//8.1e-128:550:94//AC004983

F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-sub  
unit mRNA, complete cds.//1.0e-164:777:98//AF054182

F-HEMBA1003064//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic  
sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-07:744:59//  
AC005505

F-HEMBA1003067//Rat dynorphin gene, exon 3.//1.0:140:63//M32783

F-HEMBA1003071//Homo sapiens alpha2-C4-adrenergic receptor gene, complet  
e cds.//1.5e-20:595:65//U72648

F-HEMBA1003077//CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 23  
66J21, genomic survey sequence.//4.4e-33:176:99//AQ080257

F-HEMBA1003078//Homo sapiens DNA sequence from PAC 262D12 on chromosome  
1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin,  
Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S rib  
osomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, g  
enomic marker D1S2691 and STSs.//9.4e-43:478:70//Z99297

F-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome System  
s Human BAC library) complete sequence.//0.96:57:85//AC004673

F-HEMBA1003083//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//8.0e-74:359:81//AC004548

F-HEMBA1003086//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//3.6e-11:734:58//AF001550

F-HEMBA1003096//Sequence 4 from patent US 5440017.//5.7e-56:594:71//I137  
50

F-HEMBA1003098//Human DNA sequence from cosmid SRL11M20, chromosome region 11p13. Contains EST and STS.//1.9e-09:230:69//Z83308

F-HEMBA1003117//Mouse TIS11 primary response gene, complete cds.//0.0005  
4:480:60//M58564

F-HEMBA1003129//HS\_3139\_B2\_F05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=10 Row=L, genomic survey sequence.//2.3e-100:510:97//AQ187635

F-HEMBA1003133//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//1.3e-78:370:90//AC005259

F-HEMBA1003136

F-HEMBA1003142//Homo sapiens full length insert cDNA clone ZC39B06.//6.9  
e-121:563:100//AF086197

F-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//6.7e-183:850:9  
9//AJ005670

F-HEMBA1003166//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4  
complete genomic sequence, complete sequence.//3.8e-27:229:76//AC002302

F-HEMBA1003175//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, WORKING DRAFT SEQUENCE.//9.4e-09:837:58//AB0  
00882

F-HEMBA1003179//Homo sapiens DNA sequence from Fosmid 27C3 on chromosome 22q11.2-qter. Contains two possibly alternatively spliced unknown genes, one with homology to a worm protein. Contains ESTs, complete sequence.//5.4e-115:174:98//AL022325

F-HEMBA1003197//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//1.1e-05:473:59//AC005824

F-HEMBA1003199//Rattus norvegicus Sprague-Dawley thyroid hormone receptor alpha gene, exon 1.//1.6e-05:367:61//U09302

F-HEMBA1003202//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//9.0e-23:247:73//AC004003

F-HEMBA1003204//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//4.7e-26:141:83//Z83824

F-HEMBA1003212//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSR L140b8, complete sequence.//1.9e-31:158:86//AC002037

F-HEMBA1003220//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.4e-24:284:75//AC004150

F-HEMBA1003222//RPCI11-47P17.TJ RPCI11 Homo sapiens genomic clone R-47P17, genomic survey sequence.//8.7e-39:202:99//AQ202885

F-HEMBA1003229//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone : MEB5, complete sequence.//0.86:227:62//AB019230

F-HEMBA1003235//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.6e-05:372:61//AE001373

F-HEMBA1003250//HS-1063-A1-H02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 796 Col=3 Row=0, genomic survey sequence.//0.00032:57:96//B46142

F-HEMBA1003257//H.sapiens mRNA for RDC-1 POU domain containing protein.//2.2e-08:531:59//X64624

F-HEMBA1003273//H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6 pA19H4.//0.070:267:64//Z78949

F-HEMBA1003276//CIT-HSP-2301B4.TF CIT-HSP Homo sapiens genomic clone 230 1B4, genomic survey sequence.//5.2e-08:295:63//AQ015073

F-HEMBA1003278//HS\_3075\_A1\_G09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=M, genomic survey

sequence.//0.98:399:58//AQ120599

F-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.8e-101:277:97//AC005840

F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds.//9.0e-145:539:97//AF038662

F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//5.0e-166:799:98//AB011109

F-HEMBA1003296//CITBI-E1-2507M8.TR CITBI-E1 Homo sapiens genomic clone 2 507M8, genomic survey sequence.//1.9e-05:388:63//AQ262551

F-HEMBA1003304//Budworm mitochondrial partial transfer RNA-Met (tRNA-Met) gene, and partial 12S ribosomal RNA (12S rRNA) gene.//8.0e-05:388:62//L17343

F-HEMBA1003309//Crassostrea gigas clone CN20 microsatellite sequence.//0.0017:210:64//AF051177

F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//4.6e-188:865:99//AB001872

F-HEMBA1003322//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//2.4e-54:316:87//Z93015

F-HEMBA1003327//CIT-HSP-2024C24.TRB CIT-HSP Homo sapiens genomic clone 2 024C24, genomic survey sequence.//8.4e-12:166:76//B67147

F-HEMBA1003328//HS\_2230\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=16 Row=P, genomic survey sequence.//0.026:128:71//AQ153313

F-HEMBA1003330//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//4.0e-160:745:99//AF045555

F-HEMBA1003348//HS\_3194\_A1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=M, genomic survey sequence.//5.0e-79:381:99//AQ173779

F-HEMBA1003369//H.vulgare GAA-satellite DNA.//0.12:89:71//Z50100

F-HEMBA1003370//*Homo sapiens* cosmid 123E15, complete sequence.//3.5e-32:  
199:80//AF024533

F-HEMBA1003373//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 537K23, WORKING DRAFT SEQUENCE.//0.019:117:71//AL034405

F-HEMBA1003376//Human clone HS4.66 Alu-Ya5 sequence.//4.2e-30:196:85//U6  
7229

F-HEMBA1003380//*Homo sapiens* DNA sequence from clone 394P21 on chromosome  
1p36.12-36.13. Contains the PAX7 gene, locus D1S2644, ESTs and STSs, c  
omplete sequence.//4.6e-22:206:81//AL021528

● F-HEMBA1003384//*Homo sapiens* clone GS096J14, WORKING DRAFT SEQUENCE, 3 u  
nordered pieces.//0.00094:72:90//AC006026

F-HEMBA1003395//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from MAL1P1, WORKING DRAFT SEQUENCE.//0.00041:826:57//AL031744

F-HEMBA1003402//CIT-HSP-2339K16.TR CIT-HSP *Homo sapiens* genomic clone 23  
39K16, genomic survey sequence.//2.4e-05:265:64//AQ056234

F-HEMBA1003403//*Homo sapiens* chromosome 4 clone B353C18 map 4q25, comple  
te sequence.//4.3e-135:780:90//AC004066

F-HEMBA1003408

● F-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.  
2-12.3 Contains EST, GSS, complete sequence.//1.9e-41:239:95//AL031321

F-HEMBA1003418//*Rattus norvegicus* Wistar polymeric immunoglobulin recept  
or (PIGR) gene, 3' UTR and trinucleotide repeat microsatellites.//2.2e-06  
:247:64//U08273

F-HEMBA1003433//*Homo sapiens* nibrin (NBS) mRNA, complete cds.//1.4e-149:  
697:99//AF051334

F-HEMBA1003447//*Homo sapiens* chromosome 4 clone B353C18 map 4q25, comple  
te sequence.//1.7e-77:461:90//AC004066

F-HEMBA1003461//*Rhodobacter sphaeroides* FliH (fliH) gene, partial cds, F  
liI (fliI) and FliJ (fliJ) genes, complete cds.//8.6e-08:752:58//U31090

F-HEMBA1003463//*Homo sapiens* chromosome 17, clone HCIT305D20, complete sequence.//0.089:172:68//AC004098

F-HEMBA1003480//*Homo sapiens* clone NH0523H20, complete sequence.//4.5e-150:562:97//AC005041

F-HEMBA1003528//*Streptomyces fradiae* gene for trypsinogen precursor, complete cds.//4.7e-09:433:60//D16687

F-HEMBA1003531//*Homo sapiens* PAC clone DJ1185I07 from 7q11.23-q21, complete sequence.//2.3e-48:297:90//AC004990

F-HEMBA1003538//Human complement C1r mRNA, complete cds.//4.3e-22:474:63//M14058

F-HEMBA1003545//*Rattus norvegicus* (clone 1.6kB) islet-2 mRNA, complete cds.//3.5e-143:805:91//L35571

F-HEMBA1003548

F-HEMBA1003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447E6, WORKING DRAFT SEQUENCE.//3.4e-58:331:83//AL031724

F-HEMBA1003556//*Homo sapiens* Xp22-175-176 BAC GSHB-484017 (Genome System Human BAC Library) complete sequence.//6.0e-99:703:84//AC005913

F-HEMBA1003560//Bovine GTP-binding regulatory protein gamma-6 subunit mRNA, complete cds.//1.3e-99:587:89//J05071

F-HEMBA1003568//HS\_3149\_A1\_C04\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3149 Col=7 Row=E, genomic survey sequence.//4.1e-05:389:57//AQ166810

F-HEMBA1003569//*Homo sapiens* BAC clone NH0335J18 from 2, complete sequence.//1.6e-102:669:85//AC005539

F-HEMBA1003571//*Dictyostelium discoideum* RegA (regA) gene, complete cds.//0.00033:649:58//U60170

F-HEMBA1003579//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00034:623:56//AL031744

F-HEMBA1003581//Mouse mRNA for talin.//3.3e-41:181:86//X56123

F-HEMBA1003591//*Homo sapiens* chromosome 16, BAC clone RPCI-11\_192K18 , complete sequence.//4.4e-70:273:94//AC006075

F-HEMBA1003595//*Plasmodium falciparum* chromosome 2, section 32 of 73 of the complete sequence.//6.0e-17:768:58//AE001395

F-HEMBA1003597//*Plasmodium falciparum* chromosome 2, section 35 of 73 of the complete sequence.//4.0e-09:777:56//AE001398

F-HEMBA1003598//*Homo sapiens* PAC clone DJ0537P09 from 7p11.2-p12, complete sequence.//1.3e-146:692:98//AC005153

F-HEMBA1003615//HS\_2010\_A2\_A07\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2010 Col=14 Row=A, genomic survey sequence.//1.1e-22:137:97//AQ226592

F-HEMBA1003617//*Homo sapiens* HRIHFB2157 mRNA, partial cds.//2.4e-169:501:97//AB015344

F-HEMBA1003621//*Mus musculus* PIAS3 mRNA, complete cds.//4.7e-37:165:92//AF034080

F-HEMBA1003622//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0024:514:58//AC005139

F-HEMBA1003630//CIT-HSP-2168N15.TR CIT-HSP *Homo sapiens* genomic clone 21 68N15, genomic survey sequence.//6.5e-15:358:63//B92984

F-HEMBA1003637//*Homo sapiens* clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.0e-21:238:76//AC005077

F-HEMBA1003640//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 112K5, WORKING DRAFT SEQUENCE.//2.3e-15:371:63//Z85987

F-HEMBA1003645//*A.thaliana* 81kb genomic sequence.//1.0:529:57//X98130

F-HEMBA1003646

F-HEMBA1003656

F-HEMBA1003662//*Homo sapiens* chromosome 17, clone hRPK.332\_H\_18, complete sequence.//1.6e-175:824:98//AC005746

F-HEMBA1003667//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE,  
21 unordered pieces.//1.1e-24:190:87//AC004765

F-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete se  
quence.//1.7e-162:579:99//AC005065

F-HEMBA1003680//H.sapiens DNA sequence.//7.3e-22:172:87//Z22322

F-HEMBA1003684//H.sapiens mRNA for Miz-1 protein.//0.0054:146:70//Y09723

F-HEMBA1003690//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds  
.//2.9e-72:606:77//AF039691

F-HEMBA1003692

F-HEMBA1003711//Homo sapiens chromosome 17, clone HRPC41C23, complete se  
quence.//0.55:450:60//AC003101

F-HEMBA1003714

F-HEMBA1003715//Human DNA sequence from clone 931E15 on chromosome Xq25.  
Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0  
e-16:316:68//AL023575

F-HEMBA1003720//Homo sapiens chromosome 4 clone B227H22 map 4q25, comple  
te sequence.//1.3e-41:483:73//AC004056

F-HEMBA1003725//CIT-HSP-2351H9.TF CIT-HSP Homo sapiens genomic clone 235  
1H9, genomic survey sequence.//1.1e-112:532:99//AQ079348

F-HEMBA1003729//HS\_3043\_A1\_E07\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3043 Col=13 Row=I, genomic survey  
sequence.//1.6e-12:87:98//AQ129345

F-HEMBA1003733//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.7  
e-104:761:82//AC006213

F-HEMBA1003742//HS\_3027\_A2\_B02\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3027 Col=4 Row=C, genomic survey s  
equence.//3.4e-08:67:97//AQ154731

F-HEMBA1003758//CIT-HSP-2379D18.TR CIT-HSP Homo sapiens genomic clone 23  
79D18, genomic survey sequence.//2.9e-10:310:63//AQ113513

F-HEMBA1003760//*Mus musculus* hypoxia inducible factor three alpha mRNA, complete cds.//6.4e-114:714:86//AF060194

F-HEMBA1003773//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.078:378:58//AC005139

F-HEMBA1003783//Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS.//9.0e-135:804:89//Z99496

F-HEMBA1003784//*Caenorhabditis elegans* cosmid C55B6.//0.054:463:58//U88181

F-HEMBA1003799//*Homo sapiens* Chromosome 22q11.2 Cosmid Clone 105a In DGC R Region, complete sequence.//1.9e-44:425:76//AC000070

F-HEMBA1003803//*Oryctolagus cuniculus* troponin T cardiac isoform mRNA, 3' end of cds.//0.95:198:62//L40178

F-HEMBA1003804//*Homo sapiens* chromosome 17, clone hCIT.175\_E\_5, complete sequence.//1.2e-138:275:99//AC004596

F-HEMBA1003805//*Mus musculus* quaking type I (QKI) mRNA, complete cds.//6.6e-148:753:95//U44940

F-HEMBA1003807//HS-1068-B1-G06-MR.abi CIT Human Genomic Sperm Library C *Homo sapiens* genomic clone Plate=CT 278 Col=11 Row=N, genomic survey sequence.//6.7e-07:241:67//B47212

F-HEMBA1003827//*Homo sapiens* mRNA for KIAA0616 protein, partial cds.//1.0e-83:586:87//AB014516

F-HEMBA1003836//*S.cerevisiae* chromosome IX cosmid 9150.//5.1e-16:368:63//Z38125

F-HEMBA1003838//CIT-HSP-384J15.TR CIT-HSP *Homo sapiens* genomic clone 384J15, genomic survey sequence.//1.4e-45:180:90//B54810

F-HEMBA1003856//*Homo sapiens* chromosome 10 clone CIT987SK-1188B12 map 10 p12.1, complete sequence.//0.0014:574:58//AC005875

F-HEMBA1003864//, complete sequence.//2.1e-91:234:95//AC005300

F-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds.//5.9e-81  
:853:71//AF030430

F-HEMBA1003879//H.sapiens CBP80 mRNA.//2.0e-08:87:95//X80030

F-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/  
28, WORKING DRAFT SEQUENCE.//1.7e-180:853:98//AP000036

F-HEMBA1003885//Homo sapiens PAC clone DJ0167F23 from 7p15, complete seq  
uence.//4.5e-39:376:67//AC004079

F-HEMBA1003893//H.sapiens CpG island DNA genomic MseI fragment, clone 11  
b6, forward read cpg11b6.ft1a.//3.6e-32:173:99//Z59012

F-HEMBA1003902//RPCI11-26M20.TPB RPCI-11 Homo sapiens genomic clone RPCI  
-11-26M20, genomic survey sequence.//8.2e-12:422:61//AQ003455

F-HEMBA1003908//Plasmodium falciparum chromosome 2, section 38 of 73 of  
the complete sequence.//0.0063:468:58//AE001401

F-HEMBA1003926//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 310013, WORKING DRAFT SEQUENCE.//3.6e-27:278:76//AL031658

F-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//1.4e-55:  
315:81//AF109718

F-HEMBA1003939//HS-1047-A1-G04-MF.abi CIT Human Genomic Sperm Library C  
Homo sapiens genomic clone Plate=CT 830 Col=7 Row=M, genomic survey sequ  
ence.//6.1e-09:413:63//B38195

F-HEMBA1003942//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 geno  
mic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.42:205:65/  
/AC005140

F-HEMBA1003950//M.capricolum DNA for CONTIG MC072.//0.029:458:58//Z33058

F-HEMBA1003953//HS\_2268\_A1\_B04\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2268 Col=7 Row=C, genomic survey s  
equence.//9.0e-07:239:64//AQ085098

F-HEMBA1003958//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, compl

ete sequence.//2.8e-57:424:74//AC004894

F-HEMBA1003959//RPCI11-78E8.TV RPCI11 Homo sapiens genomic clone R-78E8,  
genomic survey sequence.//4.3e-86:441:96//AQ285498

F-HEMBA1003976//HS\_3146\_A1\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=17 Row=0, genomic survey sequence.//6.3e-10:129:80//AQ141146

F-HEMBA1003978

F-HEMBA1003985//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y105C5, WORKING DRAFT SEQUENCE.//1.0:258:60//Z98855

F-HEMBA1003987

F-HEMBA1003989//*Streptomyces coelicolor* cosmid 1A9.//0.40:238:61//AL0344  
46

F-HEMBA1004000//*Rattus norvegicus* satellite sequence d0Mco2.//2.0e-07:11  
6:70//U19354

F-HEMBA1004011//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.098:286:60//AC004710

F-HEMBA1004012//*Homo sapiens* chromosome 17, clone hRPK.63\_A\_1, complete sequence.//2.8e-185:896:97//AC005670

F-HEMBA1004015//*Homo sapiens* chromosome 17, clone hRPK.721\_K\_1, complete sequence.//6.3e-68:417:80//AC005411

F-HEMBA1004024//*Homo sapiens* Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.//2.0e-47:418:77//AC005859

F-HEMBA1004038//*Homo sapiens* genomic DNA, chromosome 21q11.1, segment 23 /28, WORKING DRAFT SEQUENCE.//1.6e-51:564:74//AP000052

F-HEMBA1004042//*Plasmodium falciparum* chromosome 2, section 35 of 73 of the complete sequence.//1.2e-05:636:55//AE001398

F-HEMBA1004045//*Homo sapiens* (subclone 1\_g7 from BAC H76) DNA sequence, complete sequence.//1.9e-31:373:76//AC002252

F-HEMBA1004048//Homo sapiens DNA for P35-related protein, exon 2.//0.039  
:234:63//D63393

F-HEMBA1004049//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.//4.8e-135:780:89//AC003106

F-HEMBA1004055//Human chromosome 3p21.1 gene sequence.//4.7e-09:457:58//  
L13435

F-HEMBA1004056//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING DRAFT SEQUENCE.//3.3e-25:246:77//AL021977

F-HEMBA1004074//CIT-HSP-2053J5.TF CIT-HSP Homo sapiens genomic clone 205  
3J5, genomic survey sequence.//7.8e-24:233:76//B68555

F-HEMBA1004086//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Varlp (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//4.5e-08:614:59//U49822

F-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//5.9e-121:502:85//AF091234

F-HEMBA1004111//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.0e-36:317:80//AC006160

F-HEMBA1004131//Mus musculus clone OST2067, genomic survey sequence.//8.  
7e-24:320:71//AF046393

F-HEMBA1004132//HS\_3226\_B1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3226 Col=19 Row=H, genomic survey sequence.//9.7e-13:232:71//AQ182017

F-HEMBA1004133

F-HEMBA1004138//HS\_3036\_B1\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=N, genomic survey sequence.//0.0035:165:64//AQ294763

F-HEMBA1004143

F-HEMBA1004146

F-HEMBA1004150//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//0.00011:618:60//Z96811

F-HEMBA1004164//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome System Human BAC Library) complete sequence.//2.9e-30:454:68//AC005913

F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//4.5e-133:649:97//AF067855

F-HEMBA1004199

F-HEMBA1004200//HS\_2015\_A1\_B05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2015 Col=9 Row=C, genomic survey sequence.//8.5e-34:236:87//AQ247957

F-HEMBA1004202//Mus musculus chromosome 11, clone mCIT.268\_P\_23, complete sequence.//7.8e-59:216:83//AC004807

F-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//6.3e-98:173:98//AC005488

F-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.2e-166:791:98//U50748

F-HEMBA1004225//Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence.//6.5e-08:584:60//AE001424

F-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//8.0e-115:713:86//AF095927

F-HEMBA1004238

F-HEMBA1004241//CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence.//0.57:552:58//AC004708

F-HEMBA1004246//Human DNA sequence from clone 422F24 on chromosome 6q24. 1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//6.1e-21:254:77//AL031010

F-HEMBA1004248//Rattus rattus insulin-induced growth-respons protein (CL-6) mRNA, complete cds.//1.7e-30:315:74//L13619

F-HEMBA1004264//Homo sapiens cosmid clone LUCA20 from 3p21.3, complete s

equence.//4.4e-07:674:60//AC004693

F-HEMBA1004267//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//3.1e-78:335:87//AC004707

F-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.4e-176:856:97//AC005831

F-HEMBA1004274//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993

F-HEMBA1004275//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 501A4, WORKING DRAFT SEQUENCE.//5.2e-17:109:99//Z98051

F-HEMBA1004276//CIT-HSP-2387K6.TF.1 CIT-HSP Homo sapiens genomic clone 2 387K6, genomic survey sequence.//5.0e-07:63:98//AQ240477

F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//2.1e-185:868:99//AF022795

F-HEMBA1004289//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MQN23, complete sequence.//1.0:387:59//AB013395

F-HEMBA1004295//Homo sapiens DNA, anonymous heat-stable fragment RP11-3A .//7.8e-06:92:89//AB012254

F-HEMBA1004306//Homo sapiens clone DJ0811N16, complete sequence.//0.0003 7:413:59//AC004897

F-HEMBA1004312//Rickettsia prowazekii strain Madrid E, complete genome; segment 2/4.//0.28:522:57//AJ235271

F-HEMBA1004321//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-136:548:92//AC006130

F-HEMBA1004323//Human DNA sequence from PAC 450C20 on chromosome X.//1.3 e-32:320:65//Z84720

F-HEMBA1004327//Homo sapiens mRNA for KIAA0522 protein, partial cds.//0. 93:222:62//AB011094

F-HEMBA1004330//Homo sapiens clone DJ1196H06, WORKING DRAFT SEQUENCE, 4  
unordered pieces.//7.0e-168:895:93//AC004995

F-HEMBA1004334//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library  
) complete sequence.//4.6e-73:713:75//AC002980

F-HEMBA1004335//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 417M14, WORKING DRAFT SEQUENCE.//1.3e-25:121:85//AL024498

F-HEMBA1004341

F-HEMBA1004353//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequenc  
e.//6.4e-38:278:85//U14571

● F-HEMBA1004354//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively  
spliced, complete cds.//4.1e-45:190:92//U75968

F-HEMBA1004356

F-HEMBA1004366//P.falciparum complete gene map of plastid-like DNA (IR-A  
)//2.2e-07:736:57//X95275

F-HEMBA1004372//H.sapiens dystrophin gene intron 44.//1.0:129:62//X77644

F-HEMBA1004389//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//  
4.7e-42:237:94//M21977

F-HEMBA1004394//Plasmodium falciparum chromosome 2, section 39 of 73 of  
the complete sequence.//5.2e-05:519:59//AE001402

● F-HEMBA1004396//Human BAC clone RG302F04 from 7q31, complete sequence.//  
4.0e-32:261:76//AC002463

F-HEMBA1004405//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 geno  
mic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.4e-07:693:5  
8//AC005507

F-HEMBA1004408//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7  
unordered pieces.//1.2e-69:195:100//AC005037

F-HEMBA1004429//HS\_3193\_A1\_B06\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3193 Col=11 Row=C, genomic survey  
sequence.//5.1e-67:386:91//AQ172942

F-HEMBA1004433//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//3.2e-27:242:82//AC002554

F-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.7e-75:590:81//AC004846

F-HEMBA1004461//Human DNA sequence from clone 657J8 on chromosome Xq26.1 -26.3 Contains GSS, complete sequence.//0.045:215:66//AL034407

F-HEMBA1004479//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//5.2e-43:364:79//AF060194

F-HEMBA1004482//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//6.8e-17:791:59//AC005505

F-HEMBA1004499//Homo sapiens chromosome 17, clone hRPC.1073\_F\_15, complete sequence.//4.4e-125:251:94//AC004686

F-HEMBA1004502//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.012:635:57//AC004709

F-HEMBA1004506//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.8e-127:766:88//AC004453

F-HEMBA1004507

F-HEMBA1004509//Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project).//1.0e-13:244:67//AL021712

F-HEMBA1004534//Human mRNA for actin-binding protein (filamin) (ABP-280) .//1.6e-72:678:74//X53416

F-HEMBA1004538//Sequence 1 from patent US 5612190.//0.00015:416:59//I368

71

F-HEMBA1004542//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.95:202:64//AC005038

F-HEMBA1004554//Arabidopsis thaliana BAC T26D22.//0.45:624:56//AF058826

F-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//9.1e-10:173

:70//D87457

F-HEMBA1004573//Human BAC clone RG114A06 from 7q31, complete sequence.//  
6.1e-23:134:73//AC002542

F-HEMBA1004577//Homo sapiens Chromosome 16 BAC clone CIT987SK-582J2, complete sequence.//1.6e-15:190:77//AC004525

F-HEMBA1004586//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.1e-31:388:76//AC004895

F-HEMBA1004596//RPCI11-81021.TJ RPCI11 Homo sapiens genomic clone R-81021, genomic survey sequence.//2.2e-90:458:90//AQ285136

F-HEMBA1004604//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//8.6e-105:699:84//AF071316

F-HEMBA1004610//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//5.4e-20:267:72//AC004983

F-HEMBA1004617//CIT-HSP-2319H15.TF CIT-HSP Homo sapiens genomic clone 2319H15, genomic survey sequence.//6.2e-26:147:99//AQ034944

F-HEMBA1004629//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.6e-06:766:56//AC005504

F-HEMBA1004631//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs.//4.7e-73:412:92//Z83843

F-HEMBA1004632//Canine herpesvirus DNA for gene homolog of HSV1 UL16, EH V1 ORF 46, VZV ORF 44.//0.92:181:61//X90418

F-HEMBA1004637//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//7.8e-47:784:65//X74904

F-HEMBA1004638//Rattus norvegicus homeodomain protein Nkx6.1 (nkx6.1) mRNA, complete cds.//6.4e-06:458:61//AF004431

F-HEMBA1004666//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\* \* from clone Y47D3, WORKING DRAFT SEQUENCE.//0.30:733:55//Z98865

F-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.

1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//7.5e-136:521:98//AL031432

F-HEMBA1004670//Homo sapiens Chromosome 22q12 Cosmid Clone p90g5, complete sequence.//0.43:365:59//AC000045

F-HEMBA1004672

F-HEMBA1004693//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.096:651:54//AC005308

● F-HEMBA1004697//CIT-HSP-2326C13.TR CIT-HSP Homo sapiens genomic clone 23 26C13, genomic survey sequence.//0.23:238:65//AQ040642

F-HEMBA1004705//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPCI1-93D11 (from Roswell Park Cancer Center) complete sequence.//2.1e-27:375:72//AC002357

F-HEMBA1004709//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.6e-36:191:91//AC006210

F-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//1.1e-133:639:99//AC005562

● F-HEMBA1004725//RPCI11-75013.TJ RPCI11 Homo sapiens genomic clone R-7501 3, genomic survey sequence.//6.2e-32:169:100//AQ266512

F-HEMBA1004730//Human BAC clone RG035E18 from 7q31, complete sequence.//8.0e-68:732:72//AC004029

F-HEMBA1004733//CIT-HSP-2305M23.TF CIT-HSP Homo sapiens genomic clone 23 05M23, genomic survey sequence.//4.9e-18:209:69//AQ017556

F-HEMBA1004734//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//1.8e-13:451:62//AF028340

F-HEMBA1004736//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juve

nile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//5.0  
e-87:646:78//Z94056

F-HEMBA1004748//Human BAC clone RG204I16 from 7q31, complete sequence.//  
0.24:526:57//AC002461

F-HEMBA1004751//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6  
unordered pieces.//1.4e-25:268:76//AC004913

F-HEMBA1004752//R. norvegicus mRNA for leucocyte common antigen-related p  
rotein (3941 bp).//1.1e-07:503:61//X83546

F-HEMBA1004753//Homo sapiens Chromosome 12 Cosmid Clone 6e5, complete se  
quence.//4.5e-38:314:81//AC000028

F-HEMBA1004756//Homo sapiens, complete sequence.//1.4e-111:326:84//AC005  
854

F-HEMBA1004758//Sequence 29 from patent US 5534410.//3.9e-135:769:91//I2  
3472

F-HEMBA1004763//Homo sapiens apoptosis inhibitor survivin gene, complete  
cds.//3.6e-47:404:79//U75285

F-HEMBA1004768//Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete  
sequence.//6.7e-107:890:78//AC004941

F-HEMBA1004770//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomi  
c sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-09:806:59/  
/AC004709

F-HEMBA1004771//G. muris ribosomal RNA operon DNA encoding 16S, 23S and 5  
.8S ribosomal RNA.//0.69:239:61//X65063

F-HEMBA1004776

F-HEMBA1004778

F-HEMBA1004795//Drosophila melanogaster A-kinase anchor protein DAKAP550  
mRNA, partial cds.//3.4e-46:778:64//AF003622

F-HEMBA1004803//Homo sapiens chromosome Y, clone 264,M,20, complete sequ  
ence.//4.3e-82:580:82//AC004617

F-HEMBA1004806//*Homo sapiens* BAC clone RG281G05 from 7p15-p21, complete sequence.//5.4e-07:642:59//AC005083

F-HEMBA1004807//*Human* HIV1 tata element modulatory factor mRNA sequence from chromosome 3.//1.4e-46:171:92//L01042

F-HEMBA1004816//*Homo sapiens* calpastatin (CAST) gene, exons 10-14.//3.5e-31:546:66//M86257

F-HEMBA1004820//*C.botulinum* progenitor toxin complex genes.//0.0014:343:62//X87972

F-HEMBA1004847//*Canine* mRNA for 68kDA subunit of signal recognition particle (SRP68).//1.5e-85:512:88//X53744

F-HEMBA1004850//*Homo sapiens* TGF-beta type I receptor (TGFBR1) gene, exon 1.//0.0065:284:61//AF054590

F-HEMBA1004863//Genomic sequence from *Mouse* 11, complete sequence.//0.92:250:59//AC000400

F-HEMBA1004864

F-HEMBA1004865//*Human* DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//3.6e-12:214:72//AL031120

F-HEMBA1004880//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//1.1e-08:255:69//AC004020

F-HEMBA1004889//*Schistocerca americana* Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.062:155:69//U32943

F-HEMBA1004900//*Plasmodium falciparum* unidentified mRNA sequence.//0.00055:323:60//L12043

F-HEMBA1004909//*Homo sapiens* chromosome 17, clone 289A8, complete sequence.//9.6e-16:166:80//AC003051

F-HEMBA1004918//*Turritella communis* mitochondrial 16S ribosomal RNA gene, partial.//0.81:146:65//M94003

F-HEMBA1004923//*Human* DNA from overlapping chromosome 19-specific cosmid

s R32543, , and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//1.4e-36:338:78//AC003006

F-HEMBA1004929//CIT-HSP-2373I16.TR CIT-HSP Homo sapiens genomic clone 23 73I16, genomic survey sequence.//2.4e-86:443:96//AQ108676

F-HEMBA1004930//Homo sapiens PAC clone DJ0608H12 from 7q21, complete sequence.//4.6e-20:219:73//AC004109

F-HEMBA1004933//HS-1003-A1-E10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 497 Col=19 Row=I, genomic survey sequence.//1.4e-28:216:85//B30726

F-HEMBA1004934//Homo sapiens chromosome 21q22.3 PAC 267010, complete sequence.//0.53:222:61//AF042091

F-HEMBA1004944//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-58:509:78//AC005482

F-HEMBA1004954//HS\_2033\_A2\_A08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=16 Row=A, genomic survey sequence.//3.7e-47:243:99//AQ229758

F-HEMBA1004956//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.048:421:58//X95276

F-HEMBA1004960//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8.//0.89:333:58//Z97343

F-HEMBA1004972

F-HEMBA1004973//RPCI11-66P8.TK RPCI11 Homo sapiens genomic clone R-66P8, genomic survey sequence.//3.5e-22:245:77//AQ238471

F-HEMBA1004977//Homo sapiens full length insert cDNA clone YZ83B08.//9.0e-11:84:98//AF086080

F-HEMBA1004978//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 23 54E10, genomic survey sequence.//0.0021:152:66//AQ075713

F-HEMBA1004980//HS\_3018\_A2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=8 Row=I, genomic survey s

equence.//1.9e-77:392:97//AQ071873

F-HEMBA1004983//Albinaria corrugata isolate cor.Prn1.1 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//0.00 30:276:61//AF031680

F-HEMBA1004995//Homo sapiens chromosome 16, cosmid bridge clone 306E6 (L ANL), complete sequence.//4.2e-138:640:99//AC005590

F-HEMBA1005008//Human mariner1 transposase gene, complete consensus sequence.//6.8e-20:160:88//U52077

F-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//2.0e-1 44:668:99//AF041474

F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//1. 4e-146:693:98//AB014548

F-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6 p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA -Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//2.2e-115:668:90//AL009179

F-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//4.6e-138:591:98//AC004596

F-HEMBA1005039//CIT-HSP-2338L5.TR CIT-HSP Homo sapiens genomic clone 233 8L5, genomic survey sequence.//3.7e-61:271:88//AQ055486

F-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//3.8e-17:218:73//Z2 2819

F-HEMBA1005050//Human Tis11d gene, complete cds.//0.079:251:63//U07802

F-HEMBA1005062//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.018:560:56//AC0 04688

F-HEMBA1005066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 774G10, WORKING DRAFT SEQUENCE.//3.4e-97:432:84//AL034410

F-HEMBA1005075//H.sapiens DNA 3' flanking simple sequence region clone w  
g2c3.//6.9e-07:176:68//X76589

F-HEMBA1005079//CIT-HSP-2325M21.TRB CIT-HSP Homo sapiens genomic clone 2  
325M21, genomic survey sequence.//2.1e-48:274:93//AQ038720

F-HEMBA1005083//HS\_2248\_B1\_D05\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2248 Col=9 Row=H, genomic survey s  
equence.//3.4e-06:230:64//AQ129575

F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete  
cds.//1.3e-161:762:98//AF080561

F-HEMBA1005113//L.esculentum microsatellite repeat DNA region.//0.0038:7  
42:57//X90770

F-HEMBA1005123//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33  
unordered pieces.//9.6e-83:479:78//AC004854

F-HEMBA1005133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone Y313F4, WORKING DRAFT SEQUENCE.//3.9e-24:576:64//AL023808

F-HEMBA1005149//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, compl  
ete sequence.//4.7e-36:283:80//AC004542

F-HEMBA1005152//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUEN  
CE, 99 unordered pieces.//5.0e-10:332:64//AC004469

F-HEMBA1005159//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/  
5, WORKING DRAFT SEQUENCE.//4.0e-10:734:58//AP000023

F-HEMBA1005185//H.sapiens CpG island DNA genomic Mse1 fragment, clone 91  
b2, forward read cpg91b2.ft1a.//2.2e-14:93:100//Z63847

F-HEMBA1005201//Drosophila melanogaster cosmid 152A3.//4.7e-35:679:64//A  
L009194

F-HEMBA1005202//Canine mRNA for 68kDa subunit of signal recognition part  
icle (SRP68).//6.7e-138:778:90//X53744

F-HEMBA1005206//Drosophila melanogaster Su(P) and anon-73B1 genes and pa

rtial o25 gene and Pro26 gene.//7.1e-12:376:62//AJ011320

F-HEMBA1005219//Homo sapiens mRNA for KIAA0445 protein, complete cds.//7  
.1e-05:411:60//AB007914

F-HEMBA1005223//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.5e-06:212:66//AC004542

F-HEMBA1005232//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.7e-07:625:57//  
AC005308

F-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//8.7e-45:567:72//AC005154

F-HEMBA1005244//Homo sapiens chromosome X clone U177G4, U152H5, U168D5, 174A6, U172D6, and U186B3 from Xp22, complete sequence.//0.96:298:62//AC  
002365

F-HEMBA1005251

F-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//4.5e-160:392:99//AC005837

F-HEMBA1005274//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//2.3e-05:496:60//AF069291

F-HEMBA1005275//Human DNA sequence from clone 444C7 on chromosome 6p22.3  
-23. Contains an EST, an STS and GSSs, complete sequence.//5.7e-05:220:6  
4//AL033521

F-HEMBA1005293//Homo sapiens echinoderm microtubule-associated protein h homolog HuEMAP mRNA, complete cds.//2.4e-20:338:65//U97018

F-HEMBA1005296

F-HEMBA1005304//Human DNA sequence from clone 364I22 on chromosome Xq21.  
31-22.3. Contains an STS and GSSs, complete sequence.//1.6e-51:381:78//A  
L031012

F-HEMBA1005311

F-HEMBA1005314//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/

28, WORKING DRAFT SEQUENCE.//0.94:226:63//AP000031

F-HEMBA1005315//*Homo sapiens* BAC810, complete sequence.//9.5e-15:684:62//  
/U85198

F-HEMBA1005318//Human DNA sequence from PAC 394F12 on chromosome X contains EST, STS, CpG island clone.//2.6e-05:472:59//Z83823

F-HEMBA1005331//*Homo sapiens* chromosome 17, clone hRPK.214\_C\_8, complete sequence.//3.3e-90:300:90//AC005803

F-HEMBA1005338//*Homo sapiens* mRNA for matrilin-4, partial.//1.4e-151:740  
:97//AJ007581

F-HEMBA1005353//CIT-HSP-2310N10.TR CIT-HSP *Homo sapiens* genomic clone 23  
10N10, genomic survey sequence.//2.1e-86:438:97//AQ016145

F-HEMBA1005359//Human zinc finger protein ZNF137 mRNA, complete cds.//1.  
8e-98:500:88//U09414

F-HEMBA1005367//*Mus musculus* melastatin mRNA, complete cds.//8.3e-72:577  
:73//AF047714

F-HEMBA1005372//Human DNA sequence from PAC 293E14 contains ESTs, STS.//  
1.3e-07:274:66//Z82900

F-HEMBA1005374//*Homo sapiens* clone 277F10, WORKING DRAFT SEQUENCE, 5 uno  
rdered pieces.//1.9e-48:611:69//AC004813

F-HEMBA1005382//HS\_3063\_B2\_F11\_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//1.6e-27:154:98//AQ103204

F-HEMBA1005389//*Plasmodium falciparum* telomere nucleotide sequence.//4.0  
e-07:443:61//M23175

F-HEMBA1005394//CIT-HSP-2368B11.TR CIT-HSP *Homo sapiens* genomic clone 23  
68B11, genomic survey sequence.//7.6e-17:225:71//AQ076749

F-HEMBA1005403//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 423B22, WORKING DRAFT SEQUENCE.//4.5e-131:278:98//AL034379

F-HEMBA1005408//HS\_3007\_B2\_G04\_MR CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=3007 Col=8 Row=N, genomic survey sequence.//8.0e-06:218:66//AQ294366

F-HEMBA1005410//Human DNA sequence from cosmid cU120E2, on chromosome X contains Lowe oculocerebrorenal syndrome (OCRL) ESTs and STS.//1.5e-41:432:76//Z73496

F-HEMBA1005411

F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//1.0e-169:537:99//AF041248

F-HEMBA1005426

F-HEMBA1005443//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-37:260:76//AC006130

F-HEMBA1005447//CIT-HSP-2173N7.TR CIT-HSP Homo sapiens genomic clone 2173N7, genomic survey sequence.//5.0e-133:631:98//B93234

F-HEMBA1005468//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//1.5e-118:868:83//AL022576

F-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//1.2e-179:838:99//AC005212

F-HEMBA1005472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//3.4e-20:187:74//AL031985

F-HEMBA1005474//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE.//4.1e-22:445:65//AP000041

F-HEMBA1005475//CIT-HSP-2322D14.TR CIT-HSP Homo sapiens genomic clone 2322D14, genomic survey sequence.//6.7e-51:269:97//AQ026941

F-HEMBA1005497//HS\_3097\_A2\_G05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3097 Col=10 Row=M, genomic survey sequence.//1.4e-66:345:96//AQ103810

F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21, compl

ete sequence.//5.4e-178:818:98//AC004957

F-HEMBA1005506//*Mus musculus* (clone 0EBF17) early B-cell factor (EBF) mRNA, complete cds.//2.6e-06:73:98//L12147

F-HEMBA1005508//*Homo sapiens*, clone hRPK.1\_A\_1, complete sequence.//0.00012:455:60//AC006196

F-HEMBA1005511//*Homo sapiens* MHC class 1 region.//3.3e-43:421:77//AF0550

66

F-HEMBA1005513//*Drosophila melanogaster* males-absent on the first (mof) gene, complete cds.//2.3e-20:352:69//U71219

F-HEMBA1005517//*Homo sapiens* DNA for (CGG)n trinucleotide repeat region, isolate E7.//2.5e-08:431:62//AJ001216

F-HEMBA1005518//*M. musculus* mRNA for paladin gene.//8.2e-90:651:81//X9938

4

F-HEMBA1005520//*Homo sapiens* clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.8e-167:755:99//AC004913

F-HEMBA1005526//*Homo sapiens* chromosome 9, clone hRPK.202\_H\_3, complete sequence.//2.4e-42:475:73//AC006241

F-HEMBA1005528//*Mus musculus* mCAF1 protein mRNA, complete cds.//1.2e-94:512:92//U21855

F-HEMBA1005530

F-HEMBA1005548//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 970A17, WORKING DRAFT SEQUENCE.//9.4e-87:422:99//AL034431

F-HEMBA1005552//*Homo sapiens* PAC clone DJ0807C15 from 7q34-q36, complete sequence.//6.1e-41:486:68//AC004743

F-HEMBA1005558//*Drosophila melanogaster* DNA sequence (P1 DS00837 (D87)), complete sequence.//2.9e-19:306:68//AC004377

F-HEMBA1005568//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0093:345:60//AC004153

F-HEMBA1005570//*Plasmodium falciparum* chromosome 2, section 44 of 73 of the complete sequence.//4.2e-09:592:59//AE001407

F-HEMBA1005576//*Homo sapiens* mRNA for KIAA0463 protein, partial cds.//5.9e-127:610:98//AB007932

F-HEMBA1005577//HS-1004-A1-E11-MR.abi CIT Human Genomic Sperm Library C *Homo sapiens* genomic clone Plate=CT 498 Col=21 Row=I, genomic survey sequence.//0.00034:254:64//B30971

F-HEMBA1005581//*Rattus norvegicus* mRNA for MEGF5, complete cds.//4.0e-57:826:65//AB011531

● F-HEMBA1005582//HS\_3242\_A1\_B07\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3242 Col=13 Row=C, genomic survey sequence.//1.1e-13:91:98//AQ211275

F-HEMBA1005583

F-HEMBA1005588//*Homo sapiens* PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//8.7e-31:283:75//AC006025

F-HEMBA1005593//*Homo sapiens* chromosome 17, clone hRPK.332\_H\_18, complete sequence.//8.3e-158:748:99//AC005746

F-HEMBA1005595//CIT-HSP-2309F14.TF CIT-HSP *Homo sapiens* genomic clone 2309F14, genomic survey sequence.//6.4e-30:194:91//AQ016527

● F-HEMBA1005606//CIT-HSP-2326I6.TR CIT-HSP *Homo sapiens* genomic clone 2326I6, genomic survey sequence.//0.0014:132:70//AQ041484

F-HEMBA1005609//*Homo sapiens* clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-33:249:85//AC005089

F-HEMBA1005616//*Homo sapiens* DNA sequence from PAC 43C13 on chromosome X q21.1-Xq21.3. rab proteins geranylgeranyltransferase component A 1 (rab escort protein 1) (REP-1) (choroideraemia protein) (TCD protein).//6.5e-29:279:69//AL009175

F-HEMBA1005621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//6.4e-90:158:87//AL031731

F-HEMBA1005627//RPCI11-34P9.TJ RPCI-11 *Homo sapiens* genomic clone RPCI-1  
1-34P9, genomic survey sequence.//0.014:168:67//AQ045110

F-HEMBA1005631//*Homo sapiens* PAC clone DJ1086D14, complete sequence.//1.  
0e-149:736:93//AC004460

F-HEMBA1005632

F-HEMBA1005634//Human DNA sequence from PAC 187N21 on chromosome 6p21.2-  
6p21.33. Contains ESTs.//6.6e-38:452:67//Z98036

F-HEMBA1005666

F-HEMBA1005670//*Homo sapiens* PAC clone DJ0665C04 from 7p14-p13, complete  
sequence.//5.1e-59:687:74//AC004850

F-HEMBA1005679//*Homo sapiens* clone DJ0425I02, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//1.0e-47:357:85//AC005478

F-HEMBA1005680

F-HEMBA1005685//RPCI11-23D19.TKBR RPCI-11 *Homo sapiens* genomic clone RPC  
I-11-23D19, genomic survey sequence.//0.99:228:63//AQ013742

F-HEMBA1005699//Human ligand for eph-related receptor tyrosine kinases (EPLG8) mRNA, complete cds.//1.4e-72:406:92//U57001

F-HEMBA1005705//Human (D21S172) DNA segment containing (CA) repeat.//0.0  
0040:190:66//X56513

F-HEMBA1005717//*Plasmodium falciparum* MAL3P1, complete sequence.//0.0099  
:260:63//Z97348

F-HEMBA1005732//Human mRNA for KIAA0003 gene, complete cds.//8.1e-19:151  
:88//D14697

F-HEMBA1005737//*Homo sapiens* PAC clone DJ1099C19 from 7q21-q22, complete  
sequence.//5.6e-15:157:79//AC005156

F-HEMBA1005746//RPCI11-63N8.TK RPCI11 *Homo sapiens* genomic clone R-63N8,  
genomic survey sequence.//1.3e-18:113:100//AQ238535

F-HEMBA1005755//*Homo sapiens* DNA sequence from PAC 95C20 on chromosome X  
p11.3-11.4. Contains STSs and the DDX7 locus with GT and GTG repeat poly

morphisms, complete sequence.//3.6e-56:764:70//Z97181

F-HEMBA1005765//Human DNA sequence from PAC 288L1 on chromosome 22q12-qt  
er contains ESTs and polymorphic CA repeat (D22S1152).//1.1e-30:275:77//  
Z82196

F-HEMBA1005780//RPCI11-74E19.TJ RPCI11 Homo sapiens genomic clone R-74E1  
9, genomic survey sequence.//0.0011:283:62//AQ268432

F-HEMBA1005813//Homo sapiens PAC clone DJ0167F23 from 7p15, complete seq  
uence.//0.14:326:61//AC004079

F-HEMBA1005815//M.musculus mRNA for skeletal muscle-specific calpain.//6  
.3e-10:706:59//X92523

F-HEMBA1005822//Mouse Bac 291G16, WORKING DRAFT SEQUENCE, 19 unordered p  
ieces.//0.87:417:56//AC003020

F-HEMBA1005829//Homo sapiens Chromosome 22q11.2 Fosmid Clone f39e1 In DG  
CR Region, complete sequence.//8.8e-42:370:79//AC000094

F-HEMBA1005834//Human DNA sequence from clone 353H6 on chromosome Xq25-2  
6.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related  
, matrix associated, actin dependent regulator of chromatin, subfamily a  
, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains  
ESTs, STSSs and GSSs, complete sequence.//2.1e-42:690:67//AL022577

F-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aE9, genomic survey  
sequence.//4.3e-07:253:59//AL018749

F-HEMBA1005853//CIT-HSP-2289L23.TR CIT-HSP Homo sapiens genomic clone 22  
89L23, genomic survey sequence.//2.2e-68:333:99//B98952

F-HEMBA1005884//Homo sapiens chromosome 5, BAC clone 78c6 (LBNL H191), c  
omplete sequence.//1.9e-57:331:87//AC005351

F-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, com  
plete sequence.//5.1e-182:864:98//AC004945

F-HEMBA1005894//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered piece  
s.//3.0e-44:340:80//AC004086

F-HEMBA1005909//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1 q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//8.3e-12:828:57//AL02102  
6

F-HEMBA1005911//Human DNA sequence from clone 1158E12 on chromosome Xp11 .23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//1.0e-44 :328:77//AL031584

F-HEMBA1005921//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//1.3e-41:431:77//AC005666

F-HEMBA1005931//Homo sapiens chromosome 12p13.3 clone RPCI4-761J14, WORKING DRAFT SEQUENCE, 60 unordered pieces.//1.1e-29:394:70//AC006086

F-HEMBA1005934//Homo sapiens PAC clone DJ1140G11 from 14q24.3, complete sequence.//8.1e-06:115:80//AC004974

F-HEMBA1005962//RPCI11-17015.TV RPCI-11 Homo sapiens genomic clone RPCI-11-17015, genomic survey sequence.//9.5e-36:315:84//B82821

F-HEMBA1005963//HS\_3055\_A1\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=I, genomic survey sequence.//9.3e-73:372:97//AQ147357

F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.3e-149:697:99//AF082516

F-HEMBA1005991//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//6.3e-07:423:60//AE001408

F-HEMBA1005999//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//3.8e-09:360:64//AC005599

F-HEMBA1006002

F-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.

//4.5e-83:495:90//AF036405

F-HEMBA1006031

F-HEMBA1006035

F-HEMBA1006036//Human (lambda) DNA for immunoglobulin light chain.//2.4e-59:652:74//D87009

F-HEMBA1006042//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.//2.1e-43:330:70//AC005386

F-HEMBA1006067//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.11:433:59//AC04153

F-HEMBA1006081

F-HEMBA1006090//, complete sequence.//4.5e-139:748:92//AC005500

F-HEMBA1006091//Homo sapiens gene encoding telethonin, exons 1 to 2, partial.//0.0091:346:62//AJ011098

F-HEMBA1006100//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//2.8e-18:180:78//AC005880

F-HEMBA1006108//Human DNA sequence from clone 889N15 on chromosome Xq22. 1-22.3. Contains part of the gene for a novel protein similar to X. laev is Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSSs, GSSs and a putative CpG island, complete sequence.//0.26:84:71//AL031177

F-HEMBA1006121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 691N24, WORKING DRAFT SEQUENCE.//5.2e-18:147:87//AL031672

F-HEMBA1006124//CIT-HSP-2355B17.TF CIT-HSP Homo sapiens genomic clone 2355B17, genomic survey sequence.//0.044:225:61//AQ058966

F-HEMBA1006130//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//8.8e-07:173:69//B55085

F-HEMBA1006138//Homo sapiens DNA sequence from PAC 454M7 on chromosome X q25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//7.5e-22: 164:75//AL022162

F-HEMBA1006142//, complete sequence.//7.9e-125:586:99//AC005500

F-HEMBA1006155//H.sapiens CpG island DNA genomic Mse1 fragment, clone 11 9b6, forward read cpg119b6.ft1a.//1.0:85:72//Z64428

F-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7 ) gene, complete cds.//1.1e-185:852:99//AF048693

F-HEMBA1006173//striatum enriched phosphatase=protein-tyrosine-phosphatase [rat, striata, mRNA, 2815 nt].//8.4e-50:642:73//S49400

F-HEMBA1006182//Homo sapiens Chromosome 15q26.1 PAC clone pDJ105i19, complete sequence.//1.4e-22:194:74//AC005318

F-HEMBA1006198

F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.6e-175:836:98 //AF070557

F-HEMBA1006248//Pinctada fucata mRNA for insoluble protein, complete cds .//8.2e-05:359:61//D86074

F-HEMBA1006252//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//0.98:397:58//AL031664

F-HEMBA1006253

F-HEMBA1006259//HS\_2231\_A1\_D10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=19 Row=G, genomic survey sequence.//1.2e-11:233:68//AQ152722

F-HEMBA1006268//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome System Human BAC library) complete sequence.//5.2e-27:156:85//AC004673

F-HEMBA1006272//Human endogenous retrovirus gag mRNA.//8.1e-115:847:80// X72791

F-HEMBA1006278//Mus musculus poly(A) polymerase VI mRNA, complete cds.//

2.1e-57:665:70//U58134

F-HEMBA1006283

F-HEMBA1006284//*Streptomyces fradiae* tylactone synthase, starter module and modules 1-7, (tylG) gene, complete cds://9.6e-06:623:60//U78289

F-HEMBA1006291//HS\_2208\_A1\_C03\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2208 Col=5 Row=E, genomic survey sequence.//1.2e-13:105:92//AQ091804

F-HEMBA1006293//Sequence 8 from patent US 5721351.//5.6e-77:580:75//I894

15

F-HEMBA1006309//*Caenorhabditis elegans* cosmid F01F1.//1.1e-21:420:63//U13070

F-HEMBA1006310//*Rattus norvegicus* cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.8e-120:748:85//AF076183

F-HEMBA1006328//*Homo sapiens* fragile X mental retardation protein (FMR-1) gene (6 alternative splices), complete cds.//1.5e-46:485:73//L29074

F-HEMBA1006334//HS-1051-B2-F01-MR.abi CIT Human Genomic Sperm Library C *Homo sapiens* genomic clone Plate=CT 773 Col=2 Row=L, genomic survey sequence.//0.0032:61:91//B40563

F-HEMBA1006344//HS-1009-A2-B02-MF.abi CIT Human Genomic Sperm Library C *Homo sapiens* genomic clone Plate=CT 331 Col=4 Row=C, genomic survey sequence.//3.3e-09:218:66//B31420

F-HEMBA1006347//*Drosophila melanogaster* males-absent on the first (mof) gene, complete cds.//1.6e-31:484:68//U71219

F-HEMBA1006349//HS-1054-A1-G06-MR.abi CIT Human Genomic Sperm Library C *Homo sapiens* genomic clone Plate=CT 776 Col=11 Row=M, genomic survey sequence.//5.4e-15:95:100//B41671

F-HEMBA1006359//Human ZNF43 mRNA.//1.4e-115:823:81//X59244

F-HEMBA1006364//Mouse mRNA for transforming growth factor-beta2.//2.7e-10:247:71//X57413

F-HEMBA1006377//*Mus musculus* chromosome 7, clone 19K5, complete sequence

//3.0e-57:401:81//AC002327

F-HEMBA1006380//CIT-HSP-2172K18.TF CIT-HSP *Homo sapiens* genomic clone 21  
72K18, genomic survey sequence.//1.3e-110:525:99//B92570

F-HEMBA1006381//HS-1045-B2-F10-MF.abi CIT Human Genomic Sperm Library C  
*Homo sapiens* genomic clone Plate=CT 828 Col=20 Row=L, genomic survey seq  
uence.//4.4e-05:163:70//B37813

F-HEMBA1006398//*Homo sapiens* 12q24.2 BAC RPCI11-360E11 (Roswell Park Can  
cer Institute Human BAC Library) complete sequence.//3.8e-62:370:86//AC0  
04806

F-HEMBA1006416//*Homo sapiens* chromosome 5, P1 clone 1041F10 (LBNL H88),  
complete sequence.//3.7e-15:157:78//AC005179

F-HEMBA1006419//Human DNA sequence from clone 71L16 on chromosome Xp11.  
Contains a probable Zinc Finger protein (pseudo)gene, an unknown putativ  
e gene, a pseudogene with high similarity to part of antigen KI-67, a pu  
tative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE puta  
tive Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island,  
ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete s  
equence.//1.2e-39:752:63//AL022165

F-HEMBA1006421//*Homo sapiens* chromosome 14q24.3 clone BAC270M14 transfor  
ming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown g  
enes.//2.4e-41:438:76//AF107885

F-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-2  
7. Contains the 3' part of the alternatively spliced gene for the human  
orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and  
zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs  
, complete sequence.//0.027:293:64//AL031781

F-HEMBA1006426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 292E10, WORKING DRAFT SEQUENCE.//1.7e-50:310:80//Z93930

F-HEMBA1006438//Liverwort *Marchantia polymorpha* chloroplast genome DNA.//

/0.051:440:59//X04465

F-HEMBA1006445//*Felis catus* ras p21 (H-ras) mRNA, partial cds.//1.0:238:

59//U62088

F-HEMBA1006446//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*

from MAL1P6, WORKING DRAFT SEQUENCE.//2.4e-05:702:58//AL031749

F-HEMBA1006461//*Homo sapiens* chromosome 19, cosmid R30676, complete sequence.//8.6e-55:409:83//AC004560

F-HEMBA1006467//*Homo sapiens* chromosome 17, clone hRPK.346\_K\_10, complete sequence.//1.0:293:59//AC006120

F-HEMBA1006471//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.4e-05:731:59//AC004709

F-HEMBA1006474//CIT-HSP-2017H3.TF CIT-HSP *Homo sapiens* genomic clone 2017H3, genomic survey sequence.//5.2e-60:435:83//B54247

F-HEMBA1006483//*Homo sapiens* chromosome 5, BAC clone 8e5 (LBNL H167), complete sequence.//2.9e-48:286:84//AC004752

F-HEMBA1006485//*Homo sapiens* BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//0.96:283:59//AC006031

F-HEMBA1006486//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.8e-14:259:67//AL022577

F-HEMBA1006489//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467K16, WORKING DRAFT SEQUENCE.//6.6e-11:595:61//AL031283

F-HEMBA1006492//*Homo sapiens* chromosome 17, clone hRPK.269\_G\_24, complete sequence.//6.0e-122:337:100//AC005828

F-HEMBA1006494//*Homo sapiens* chromosome 7qtel0 BAC E3, complete sequence

//3.8e-23:459:68//AF093117

F-HEMBA1006497//HS\_3023\_B2\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=6 Row=P, genomic survey sequence.//2.3e-81:433:95//AQ093846

F-HEMBA1006502//H.sapiens 7SL repeat (clones 2-19b).//1.6e-13:86:87//X62  
364

F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//2.  
3e-139:470:98//AB014566

F-HEMBA1006521//Human BAC clone RG167B05 from 7q21, complete sequence.//  
4.3e-27:406:71//AC003991

F-HEMBA1006530//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 1018D12, WORKING DRAFT SEQUENCE.//2.9e-27:408:65//AL031650

F-HEMBA1006535//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from MAL4P1, WORKING DRAFT SEQUENCE.//0.028:599:60//AL034557

F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA  
, complete cds.//1.4e-171:654:98//AF093419

F-HEMBA1006546//Human DNA sequence from cosmid 232L22, between markers D  
XS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene  
.//3.8e-104:811:80//Z73986

F-HEMBA1006559//*Mus musculus* PRAJA1 (Praja1) mRNA, complete cds.//4.8e-9  
9:386:82//U06944

F-HEMBA1006562//Human fructose-1,6-biphosphatase (FBP1) gene, exon 1.//0  
.012:322:60//U21925

F-HEMBA1006566//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1383 genomic  
sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0026:580:58//  
AC005504

F-HEMBA1006569//*Ovis aries* beta actin mRNA, complete cds.//6.3e-08:231:7  
0//U39357

F-HEMBA1006579//CIT-HSP-2380A22.TR CIT-HSP Homo sapiens genomic clone 23

80A22, genomic survey sequence.//0.036:250:62//AQ197107

F-HEMBA1006583//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.0:225:63//AL021841

F-HEMBA1006595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//3.6e-50:689:69//AL022156

F-HEMBA1006597//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-42:253:84//AC004166

F-HEMBA1006612//RPCI11-88F20.TJ RPCI11 Homo sapiens genomic clone R-88F20, genomic survey sequence.//1.1e-51:266:98//AQ286726

F-HEMBA1006617//HS\_2193\_B2\_H07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=14 Row=P, genomic survey sequence.//1.1e-59:413:85//AQ299685

F-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiuinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//1.4e-35:257:89//AL023284

F-HEMBA1006631//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//9.6e-112:800:83//AC002036

F-HEMBA1006635//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING DRAFT SEQUENCE.//0.15:393:58//AL031745

F-HEMBA1006639//Petromyzon marinus polyadenylate binding protein (PABP) mRNA, complete cds.//9.6e-15:318:68//AF032896

F-HEMBA1006643//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.58:254:65//AC006148

F-HEMBA1006648//Mus musculus integrin binding protein kinase mRNA, complete cds.//1.5e-37:108:88//U94479

F-HEMBA1006652//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180),

complete sequence.//1.3e-154:671:96//AC005601

F-HEMBA1006653

F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//5.2e-110:254:93//AC005189

F-HEMBA1006665//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//1.4e-14:177:76//AC004554

F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56.//5.5e-15:122:90//Y12065

F-HEMBA1006676//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//0.098:218:63//AC004755

F-HEMBA1006682//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING DRAFT SEQUENCE.//1.4e-05:719:57//AL034346

F-HEMBA1006695//Homo sapiens clone DJ0935K16, complete sequence.//3.1e-22:151:78//AC006011

F-HEMBA1006696//CITBI-E1-2522D16.TF CITBI-E1 Homo sapiens genomic clone 2522D16, genomic survey sequence.//5.6e-17:324:66//AQ280738

F-HEMBA1006708

F-HEMBA1006709

F-HEMBA1006717//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.3e-08:136:79//AC005537

F-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//5.8e-162:497:98//AC005828

F-HEMBA1006744//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//7.4e-48:320:87//AC004796

F-HEMBA1006754//Human DNA sequence from PAC 82J11 and cosmid U134E6 on chromosome Xq22. Contains NIK like and Thyroxin-binding globulin precursor (T4-binding globulin, TBG) genes, ESTs and STSs.//4.1e-129:804:85//Z83850

F-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161),

complete sequence.//2.2e-162:766:99//AC005752

F-HEMBA1006767//Human Xq28 cosmid U247A3 from LLOXNC01 X chromosome library, complete sequence.//1.2e-19:326:69//U73465

F-HEMBA1006779//Human DNA sequence from clone 80I19 on chromosome 6p21.3  
1-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//1.4e-103:355:87//AL022727

F-HEMBA1006780//CIT-HSP-2359P7.TR CIT-HSP Homo sapiens genomic clone 235  
9P7, genomic survey sequence.//0.072:147:68//AQ077208

F-HEMBA1006789//nbxb0037I13r CUGI Rice BAC Library Oryza sativa genomic  
clone nbxb0037I13r, genomic survey sequence.//0.00011:288:63//AQ290474

F-HEMBA1006795//CIT-HSP-2307E3.TF CIT-HSP Homo sapiens genomic clone 230  
7E3, genomic survey sequence.//5.1e-80:420:96//AQ020511

F-HEMBA1006796//Human clone 23803 mRNA, partial cds.//4.5e-06:202:68//U7  
9298

F-HEMBA1006807//Homo sapiens mRNA for SPOP.//1.2e-66:651:73//AJ000644

F-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62\_0\_9, complete  
sequence.//6.0e-116:541:99//AC004797

F-HEMBA1006824//Homo sapiens chromosome 19, cosmid R29368, complete sequ  
ence.//0.40:159:66//AC004262

F-HEMBA1006832//Homo sapiens (subclone 3\_g8 from P1 H25) DNA sequence, c  
omplete sequence.//1.8e-24:323:71//AC002196

F-HEMBA1006849//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat e  
pithelium cancer , segment 4/10.//0.15:403:60//AB020872

F-HEMBA1006865//Plasmodium falciparum chromosome 2, section 6 of 73 of t  
he complete sequence.//0.20:472:57//AE001369

F-HEMBA1006877//Mus musculus clone OST9241, genomic survey sequence.//3.  
4e-79:641:76//AF046757

F-HEMBA1006885//HS\_2208\_B2\_G06\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2208 Col=12 Row=N, genomic survey

sequence.//4.9e-18:206:76//AQ089246

F-HEMBA1006900//Human DNA sequence from clone 496N17 on chromosome 6p11.

2-12.3 Contains EST, GSS, complete sequence.//5.4e-07:298:65//AL031321

F-HEMBA1006914//S.pombe chromosome II cosmid c16H5.//0.00040:194:66//AL022104

F-HEMBA1006921//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//1.1e-174:813:99//AC006027

F-HEMBA1006926//Caenorhabditis elegans cosmid ZK185.//0.0075:183:65//AF036704

● F-HEMBA1006929//P.falciparum complete gene map of plastid-like DNA (IR-A).//4.0e-06:739:57//X95275

F-HEMBA1006936

F-HEMBA1006938//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P4, WORKING DRAFT SEQUENCE.//1.1e-05:733:57//AL031747

F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//1.3e-90:437:98//AJ010841

F-HEMBA1006949//Human DNA sequence from PAC 363L9 on chromosome X. contains STS and polymorphic CA repeat.//0.67:217:62//Z82205

● F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.6e-143:740:94//AF004828

F-HEMBA1006976//cDNA encoding alpha 2 to 3 sialyltransferase.//2.8e-101:338:89//E06058

F-HEMBA1006993//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//7.1e-31:536:66//AC003071

F-HEMBA1006996//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//9.5e-07:285:60//Z82209

F-HEMBA1007002//Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence.//0.99:388:58//AC002328

F-HEMBA1007017//Sequence 3 from Patent W09416067.//0.96:220:62//A39358

F-HEMBA1007018//*G.gallus* mRNA for dynein light chain-A.//1.3e-124:838:83

//X79088

F-HEMBA1007045

F-HEMBA1007051//*Caenorhabditis elegans* cosmid Y57G11C, complete sequence  
//0.17:343:60//Z99281

F-HEMBA1007052//*Homo sapiens* FSHD-associated repeat DNA, proximal region  
//4.3e-67:659:74//U85056

F-HEMBA1007062//Tubulin gene.//1.0:113:67//A18572

F-HEMBA1007066//HS\_3116\_A2\_A03\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3116 Col=6 Row=A, genomic survey sequence.//0.80:214:62//AQ140467

F-HEMBA1007073//*Homo sapiens* 12q13 PAC RPCII-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//9.3e-54:519:68//AC0042

42

F-HEMBA1007078//CIT-HSP-2318N6.TF CIT-HSP *Homo sapiens* genomic clone 2318N6, genomic survey sequence.//8.7e-80:387:98//AQ044076

F-HEMBA1007080

F-HEMBA1007085//*Streptomyces coelicolor* cosmid 7A1.//3.5e-06:496:59//AL034447

F-HEMBA1007087//*Plasmodium falciparum* MAL3P6, complete sequence.//7.4e-07:553:56//Z98551

F-HEMBA1007112//HS\_2171\_A1\_B01\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2171 Col=1 Row=C, genomic survey sequence.//1.0:172:61//AQ091865

F-HEMBA1007113//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//0.54:502:56//AL023875

F-HEMBA1007121//*Caenorhabditis elegans* cosmid ZK430.//1.4e-08:265:64//U42833

F-HEMBA1007129//CITBI-E1-2504A5.TF CITBI-E1 *Homo sapiens* genomic clone 2

504A5, genomic survey sequence.//0.97:267:62//AQ264035

F-HEMBA1007147//HS\_3208\_A2\_C04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=8 Row=E, genomic survey sequence.//9.1e-90:466:95//AQ176696

F-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//6.0e-138:524:98//AC005239

F-HEMBA1007151//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2 522H6, genomic survey sequence.//2.0e-20:157:87//AQ280780

F-HEMBA1007174//Homo sapiens epsin 2a mRNA, complete cds.//2.0e-62:318:9 7//AF062085

F-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPCI11-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//1.6e-21:205:80//AC005911

F-HEMBA1007194//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.3e-11:87:96//AQ187492

F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.7e-156:478:98//D86987

F-HEMBA1007206//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//0.024:342:63//AC004223

F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds.//5.0e-176:839:98//AB018340

F-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//4.3e-58:687:68 //J00060

F-HEMBA1007251//Rabbit troponin T messenger fragment (aa 49 to 129).//0.084:177:62//V00899

F-HEMBA1007256//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//1.3e-75:490:88//AL022240

F-HEMBA1007267//HS\_3218\_A1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=13 Row=K, genomic survey

sequence.//2.9e-62:393:87//AQ181128

F-HEMBA1007273//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 21  
71B10, genomic survey sequence.//1.1e-63:314:99//B95401

F-HEMBA1007279//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10,  
complete sequence.//3.1e-31:401:72//AC004638

F-HEMBA1007281//HS\_3115\_A1\_A11\_T7 CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=3115 Col=21 Row=A, genomic survey  
sequence.//5.0e-70:372:96//AQ186691

F-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24  
Contains EST, STS, GSS, CpG island, complete sequence.//1.2e-152:727:98/  
/AL031003

F-HEMBA1007300//Canis familiaris PDE5 mRNA for 3',5'-Cyclic GMP Phosphodiesterase, complete cds.//2.1e-21:542:63//AB008467

F-HEMBA1007301//COL1A1-type I collagen pro alpha 1(I) chain propeptide {  
3' region} [human, fetal cells 86-237, 86-146, 88-251, mRNA Partial Muta  
nt, 855 nt].//1.7e-08:388:61//S64596

F-HEMBA1007319//Genomic sequence from Mouse 9, complete sequence.//6.0e-  
84:390:75//AC000399

F-HEMBA1007320

F-HEMBA1007322//Homo sapiens BAC clone RG118E13 from 7p15-p21, complete  
sequence.//0.091:260:64//AC004485

F-HEMBA1007327//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 geno  
mic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.12:472:59/  
/AC005140

F-HEMBA1007341//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, comple  
te sequence.//1.5e-18:408:64//AC006120

F-HEMBA1007342//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4  
unordered pieces.//8.7e-25:500:62//AC005377

F-HEMBA1007347//Homo sapiens chromosome 5, BAC clone 7g12 (LBNL H126), c

omplete sequence.//0.75:269:61//AC005738

F-HEMBB1000005//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//5.0e-05:441:60//AC004617

F-HEMBB1000008//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.0e-44:417:77//AC004491

F-HEMBB1000018//HS\_2179\_B2\_E04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=8 Row=J, genomic survey sequence.//0.012:87:77//AQ023250

F-HEMBB1000024//Human DNA sequence from PAC 106I20 on chromosome 22q12-qter contains NADH pseudogene, ESTs, STS.//8.1e-11:461:61//Z81369

F-HEMBB1000025//CIT-HSP-2348F3.TR CIT-HSP Homo sapiens genomic clone 2348F3, genomic survey sequence.//0.96:198:62//AQ062938

F-HEMBB1000030//Homo sapiens DNA sequence from PAC 32F7 on chromosome X. Contains NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 3, ESTs.//0.00049:276:64//AL009173

F-HEMBB1000036//H.sapiens chromosome 22 CpG island DNA genomic MseI fragment, clone 302e2, reverse read 302e2.r.//0.0057:66:81//Z79857

F-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.9e-100:450:98//AF084928

F-HEMBB1000039//HS\_2167\_B1\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2167 Col=23 Row=L, genomic survey sequence.//0.022:108:69//AQ092404

F-HEMBB1000044//Borrelia burgdorferi (section 50 of 70) of the complete genome.//1.0e-07:486:61//AE001164

F-HEMBB1000048//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.3e-05:585:58//AC005507

F-HEMBB1000050//Homo sapiens DNA sequence from clone 501N12 on chromosome 6p22.1-22.3 Contains a gene almost identical to four genes of unknown

function, a pseudogene, three (pseudo?) genes similar to genes of unknown function, an unknown gene similar to a rat EST, a PX19 LIKE pseudogene and another unknown gene. Contains ESTs, STSs and GSSs, complete sequence.//5.8e-38:549:67//AL022170

F-HEMBB1000054//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//7.0e-98:328:83//AC002349

F-HEMBB1000055//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, cosmid clone: TY2F10, WORKING DRAFT SEQUENCE .//3.7e-05:600:58//AB000880

● F-HEMBB1000059//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.3e-48:472:78//AC005096

F-HEMBB1000083

F-HEMBB1000089//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.0036:679:56//AL031744

F-HEMBB1000099//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-15:312:68//AC005909

F-HEMBB1000103//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.0e-37:316:74//AC006210

● F-HEMBB1000113//Homo sapiens chromosome 21q22.3 cosmid Q11M15, complete sequence.//3.1e-25:259:76//AF045450

F-HEMBB1000119//Homo sapiens ASMTL gene.//1.2e-137:654:98//Y15521

F-HEMBB1000136//Mycobacterium tuberculosis H37Rv complete genome; segment 127/162.//0.59:217:66//Z74697

F-HEMBB1000141//Homo sapiens DNA from chromosome 19q13.1 cosmid f14121 containing ATP4A and GADPH-2 genes, genomic sequence.//8.4e-31:113:88//AD000090

F-HEMBB1000144//Human BAC clone RG114A06 from 7q31, complete sequence.//4.4e-58:339:87//AC002542

F-HEMBB1000173//*Homo sapiens* 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//9.4e-160:562:93//AC002996

F-HEMBB1000175

F-HEMBB1000198//HS\_3071\_A2\_A10\_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3071 Col=20 Row=A, genomic survey sequence.//0.99:261:61//AQ137388

F-HEMBB1000215//*Homo sapiens* chromosome 17, clone hRPK.481\_C\_4, complete sequence.//6.7e-17:138:86//AC005839

F-HEMBB1000217//*Arabidopsis thaliana* ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00083:287:60//U80808

F-HEMBB1000218//*Caenorhabditis elegans* cosmid C52A11, complete sequence.//0.90:337:56//Z46792

F-HEMBB1000226//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.//1.7e-90:175:92//Z69890

F-HEMBB1000240//Human G-protein-coupled inwardly rectifying potassium channel (KCNJ3) gene, polymorphic repeat sequence.//0.16:171:62//U07918

F-HEMBB1000244//*Homo sapiens* clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.8e-08:355:63//AC005522

F-HEMBB1000250//*Homo sapiens* protein associated with Myc mRNA, complete cds.//6.6e-155:735:98//AF075587

F-HEMBB1000258//Human adenosine monophosphate deaminase 1 (AMPD1) gene, exons 1-16.//0.58:396:59//M98818

F-HEMBB1000264//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds.//4.4e-32:100:100//U75968

F-HEMBB1000266//*Homo sapiens* Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//3.8e-16:176:78//AC004470

F-HEMBB1000272//*Plasmodium falciparum* chromosome 2, section 6 of 73 of t

he complete sequence.//0.011:379:58//AE001369

F-HEMBB1000274//Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project).//0.92:272:61//AL022580

F-HEMBB1000284//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics), PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//0.00071:568:57//AC002366

F-HEMBB1000307//Human DNA sequence from PAC 29K1 on chromosome 6p21.3-22.2. Contains glutathione peroxidase-like; zinc finger, ESTs, mRNA, STS, tRNAs, olfactory receptor pseudogene.//3.0e-13:439:65//Z98745

● F-HEMBB1000312//Homo sapiens clone GS051M12, complete sequence.//0.031:252:65//AC005007

F-HEMBB1000317//Fugu rubripes GSS sequence, clone 060J22aE10, genomic survey sequence.//0.00033:173:65//AL026242

F-HEMBB1000318//HS\_3244\_B2\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=20 Row=P, genomic survey sequence.//3.9e-85:438:95//AQ252951

F-HEMBB1000335//Homo sapiens chromosome 18, clone hRPK.24\_A\_23, complete sequence.//0.63:285:61//AC005968

● F-HEMBB1000336

F-HEMBB1000337//Homo sapiens chromosome 4 clone B208G5 map 4q25, complete sequence.//0.0014:309:64//AC004051

F-HEMBB1000338//HS\_3108\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=14 Row=K, genomic survey sequence.//3.8e-09:331:63//AQ140356

F-HEMBB1000339//Homo sapiens 12q24 PAC RPCI1-46F2 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-52:295:77//AC002351

F-HEMBB1000341

F-HEMBB1000343//Plasmodium falciparum MAL3P3, complete sequence.//0.00081:397:61//Z98547

F-HEMBB1000354//Human DNA sequence from clone 192P9 on chromosome Xp11.2

3-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//9.1e-34:596:66//AL020989

F-HEMBB1000369//Genomic sequence from Human 17, complete sequence.//0.01 2:298:60//AC002090

F-HEMBB1000374//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L 21) from the Roswell Park Cancer Institute, complete sequence.//9.3e-69: 294:89//U96409

F-HEMBB1000376//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence .//3.5e-54:352:88//AL034377

F-HEMBB1000391//Trichothecium roseum internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.//0.011:168:67//U51982

F-HEMBB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//2.6e-163:762:98//AF076838

F-HEMBB1000402//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//7.7e-15:466:63//AC002368

F-HEMBB1000404//Homo sapiens mRNA for myosin-IXA.//3.5e-65:324:98//AJ001 714

F-HEMBB1000420//244Kb Contig from Human Chromosome 11p15.5 spanning D11S1 through D11S25, complete sequence.//0.013:399:62//AC001228

F-HEMBB1000434//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//6.1e-83:571:84//AC004263

F-HEMBB1000438//RPCI11-21E14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21E14, genomic survey sequence.//0.0030:295:63//B83110

F-HEMBB1000441//Homo sapiens Chromosome 22q12 Cosmid Clone 1147g11, complete sequence.//2.5e-33:372:72//AC000035

F-HEMBB1000449//Human DNA sequence from PAC 296K21 on chromosome X conta

ins cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase. (EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//1.3e-51:534:72//Z83821

F-HEMBB1000455//Saccharomyces cerevisiae mitochondrion origin of replication (ori6) and oil1 gene, complete cds.//0.016:522:58//L36899

F-HEMBB1000472

F-HEMBB1000480

F-HEMBB1000487//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 12803, WORKING DRAFT SEQUENCE.//0.00013:314:64//Z98742

F-HEMBB1000490//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//4.1e-110:529:98//AL034423

F-HEMBB1000491//Plasmodium falciparum chromosome 2, section 25 of 73 of the complete sequence.//0.10:187:65//AE001388

F-HEMBB1000493//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-06:637:58//AL022577

F-HEMBB1000510//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//3.1e-96:737:81//AC005553

F-HEMBB1000518//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.00014:163:68//AC004676

F-HEMBB1000523//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-105, complete sequence.//0.41:349:56//AL010212

F-HEMBB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus.//6.6e-37:138:96//Y11710

F-HEMBB1000550//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.

//3.9e-56:683:71//AB020860

F-HEMBB1000554//*Homo sapiens* \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT  
SEQUENCE.//2.2e-51:282:84//AJ011929

F-HEMBB1000556//*Homo sapiens* mRNA for KIAA0750 protein, complete cds.//6  
.1e-32:537:65//AB018293

F-HEMBB1000564

F-HEMBB1000573//*Homo sapiens* clone RG228D17, WORKING DRAFT SEQUENCE, 2 un  
ordered pieces.//8.2e-33:268:73//AC005077

F-HEMBB1000575//Human DNA sequence from clone 323M22 on chromosome 22q13  
.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and m  
ouse H74, and a novel gene coding for a protein similar to KIAA0173 and  
worm Tubulin Tyrosine Ligase. Contains ESTS, STSs, GSSs, genomic marker  
D22S418 and putative CpG islands, complete sequence.//5.8e-47:734:66//AL  
022476

F-HEMBB1000586//*H.sapiens* highly polymorphic microsatellite DNA.//0.030:  
147:67//X79883

F-HEMBB1000589//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-A-279B10,  
complete sequence.//6.3e-41:278:83//AC002300

F-HEMBB1000591//*Homo sapiens* Xp22 bins 45-47 BAC GSHB-665N22 (Genome Sys  
tems Human BAC Library) complete sequence.//1.1e-182:871:98//AC005184

F-HEMBB1000592//Hepatitis C virus genomic RNA, 3' nontranslated region,  
partial sequence. clone #19.//0.012:185:64//AF009074

F-HEMBB1000593//*Homo sapiens* chromosome 7q22 sequence, complete sequence  
.//1.2e-131:353:93//AF053356

F-HEMBB1000598//*Homo sapiens* 12p13.3 BAC RPCI3-488H23 (Roswell Park Canc  
er Institute Human BAC Library) complete sequence.//9.1e-58:600:72//AC00  
6207

F-HEMBB1000623//cDNA encoding *Coliolum manganese peroxidase*.//0.89:284:6  
2//E12284

F-HEMBB1000630//*Mus musculus* clone NSAT47 nonsatellite RNA sequence.//1.

9e-15:129:87//U26231

F-HEMBB1000631//Sequence 26 from patent US 5708157.//3.2e-27:180:88//I80

057

F-HEMBB1000632//Human mRNA for KIAA0351 gene, complete cds.//1.6e-48:811  
:65//AB002349

F-HEMBB1000637//*Homo sapiens* clone DJ0425I02, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//4.1e-58:649:73//AC005478

F-HEMBB1000638//HS\_3051\_A1\_G01\_MF CIT Approved Human Genomic Sperm Libra  
ry D *Homo sapiens* genomic clone Plate=3051 Col=1 Row=M, genomic survey s  
equence.//0.0032:497:56//AQ155234

F-HEMBB1000643//*Homo sapiens* clone RG228D17, WORKING DRAFT SEQUENCE, 2 u  
nordered pieces.//2.4e-50:791:68//AC005077

F-HEMBB1000649//*Homo sapiens* Chromosome 16 BAC clone CIT987-SK502C10, co  
mplete sequence.//5.2e-64:775:69//AC003009

F-HEMBB1000652//*Homo sapiens* chromosome 10 clone CRI-JC2048 map 10q22.1,  
WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.7e-52:334:89//AC006186

F-HEMBB1000665//Human DNA sequence from clone 452M16 on chromosome Xq21.  
1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS  
, GSS, and CA repeat, complete sequence.//0.0062:426:60//AL024493

F-HEMBB1000671//Human DNA sequence from PAC 93H18 on chromosome 6 contai  
ns ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG isla  
nd.//9.6e-95:399:78//Z84488

F-HEMBB1000673//HS\_3039\_A2\_C08\_MF CIT Approved Human Genomic Sperm Libra  
ry D *Homo sapiens* genomic clone Plate=3039 Col=16 Row=E, genomic survey  
sequence.//3.8e-50:293:92//AQ155121

F-HEMBB1000684//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 222E13, WORKING DRAFT SEQUENCE.//8.0e-65:282:83//Z93241

F-HEMBB1000693//*Homo sapiens* neuroanl mRNA, complete cds.//1.6e-118:575:

97//AF040723

F-HEMBB1000705//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.6e-07:251:6  
1//AC005507

F-HEMBB1000706//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//2.9e-20:434:64//AL031118

F-HEMBB1000709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 994L9, WORKING DRAFT SEQUENCE.//0.26:184:65//AL034554

F-HEMBB1000725//*Rattus norvegicus* GTPase Rab8b (Rab8b) mRNA, complete cds.//1.8e-129:692:93//U53475

F-HEMBB1000726//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.7e-40:304:80//U91321

F-HEMBB1000738//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//8.9e-35:582:63//AF011889

F-HEMBB1000749//*Homo sapiens* chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.//6.2e-46:262:89//AC005849

F-HEMBB1000763//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//1.6e-99:316:98//AL034405

F-HEMBB1000770//Human DNA sequence from clone 80I19 on chromosome 6p21.3 1-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//0.044:325:60//AL022727

F-HEMBB1000774

F-HEMBB1000781//Sequence 3 from patent US 5753446.//1.2e-92:599:86//AR008277

F-HEMBB1000789//*Homo sapiens* mRNA for KIAA0677 protein, complete cds.//9.3e-64:672:71//AB014577

F-HEMBB1000790//*Homo sapiens* 12q13.1 PAC RPCI1-228P16 (Roswell Park Canc

er Institute Human PAC Library) complete sequence.//2.4e-41:460:74//AC00  
4801

F-HEMBB1000794//HS\_3034\_B2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=24 Row=H, genomic survey sequence.//1.8e-74:378:97//AQ117099

F-HEMBB1000807//H.sapiens CpG island DNA genomic Msel fragment, clone 39 d7, reverse read cpg39d7.rt1a.//8.5e-14:95:97//Z58412

F-HEMBB1000810//H.sapiens chromosome 22 CpG island DNA genomic Msel fragment, clone 303a8, complete read.//3.2e-05:138:71//Z79983

● F-HEMBB1000821//HS\_2168\_B1\_A12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=B, genomic survey sequence.//0.85:208:60//AQ086361

F-HEMBB1000822//Human BAC clone GS113H23 from 5p15.2, complete sequence.//3.0e-06:361:60//AC003015

F-HEMBB1000826//Human BAC clone RG180F08 from 7q31, complete sequence.//1.1e-27:360:69//AC002431

F-HEMBB1000827

F-HEMBB1000831

● F-HEMBB1000835//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//0.00098:234:63//AL023581

F-HEMBB1000840//Human Chromosome 11 Cosmid cSRL97a6, complete sequence.//4.5e-61:328:79//U73649

F-HEMBB1000848//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence.//9.7e-144:809:87//AL021068

F-HEMBB1000852//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.12:492:58//AC004157

F-HEMBB1000870//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0024:212:67//AC004157

F-HEMBB1000876//*Homo sapiens* ELISC-1 mRNA, partial cds.//1.5e-32:200:94//AF085351

F-HEMBB1000883//HS\_3065\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3065 Col=8 Row=F, genomic survey sequence.//0.0017:152:66//AQ137687

F-HEMBB1000887

F-HEMBB1000888//CIT-HSP-2329A10.TR CIT-HSP *Homo sapiens* genomic clone 23 29A10, genomic survey sequence.//1.5e-31:172:98//AQ044369

F-HEMBB1000890

F-HEMBB1000893//*Plasmodium falciparum* MAL3P2, complete sequence.//9.5e-0 6:768:56//AL034558

F-HEMBB1000908//*Homo sapiens* clone DJ1119N05, complete sequence.//4.5e-2 1:199:82//AC004968

F-HEMBB1000910//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.72:366:59//AL034557

F-HEMBB1000913//HS\_3078\_B1\_C02\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//9.9e-12:221:63//AQ144507

F-HEMBB1000915//*Homo sapiens* DNA for (CGG)<sub>n</sub> trinucleotide repeat region, isolate P4.//1.2e-49:252:99//AJ001215

F-HEMBB1000917//*Homo sapiens* chromosome 5, P1 clone 254f11 (LBNL H62), complete sequence.//2.3e-42:316:76//AC006077

F-HEMBB1000927//*Human* BDR-2 mRNA for hippocalcin, complete cds.//3.6e-30

:528:65//D16593

F-HEMBB1000947//CpG0856B CpIOWAgDNA1 *Cryptosporidium parvum* genomic, genomic survey sequence.//0.81:262:62//AQ254493

F-HEMBB1000959//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34606, WORKING DRAFT SEQUENCE.//1.2e-43:454:75//Z84487

F-HEMBB1000973//*Mus musculus* schlafenz2 (Slfn2) mRNA, complete cds.//8.3e-42:458:72//AF099973

F-HEMBB1000975//*Arabidopsis thaliana* genomic DNA, chromosome 5, P1 clone : MBK5, complete sequence.//0.98:196:63//AB005234

F-HEMBB1000981

F-HEMBB1000985//*Homo sapiens* chromosome 19, cosmid R29388, complete sequence.//2.9e-06:566:57//AC004476

F-HEMBB1000991//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//0.099:391:57//Z98753

F-HEMBB1000996//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-sequences (GSSs).//6.2e-33:227:80//Z94802

F-HEMBB1001004

F-HEMBB1001008//Human Chromosome 16 BAC clone CIT987SK-A-951C11, complete sequence.//4.0e-13:164:79//AC002551

F-HEMBB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//7.5e-13:229:69//AC002310

F-HEMBB1001014//*Homo sapiens* chromosome 16, BAC clone 375G12 (LANL), complete sequence.//0.32:474:58//AC005751

F-HEMBB1001020//*Homo sapiens* BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//2.6e-39:218:80//AF069291

F-HEMBB1001024//*Homo sapiens* BAC clone 393I22 from 8q21, complete sequence.//5.3e-05:656:59//AF070717

F-HEMBB1001037//CIT-HSP-2358K16.TF CIT-HSP *Homo sapiens* genomic clone 23 58K16, genomic survey sequence.//6.6e-05:228:64//AQ080539

F-HEMBB1001047//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA  
1733 and Qc17B8 from Xq28, complete sequence.//4.0e-27:385:71//U82671

F-HEMBB1001051//H.sapiens mRNA for FAN protein.//1.2e-27:160:98//X96586

F-HEMBB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//2.3e-89:180:91//AC006014

F-HEMBB1001058//Homo sapiens 3p22-8 PAC RPC14-736H12 (Roswell Park Cancer  
Institute Human PAC Library) complete sequence.//1.2e-41:468:74//AC006  
060

F-HEMBB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.3e-122:785:86//U49973

F-HEMBB1001063//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
523G1, WORKING DRAFT SEQUENCE.//7.1e-162:770:99//AL034375

F-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//3.1e-146:7  
36:95//AF034803

F-HEMBB1001096//Buchnera aphidicola genomic fragment containing (chaperone Hsp60)  
groEL, DNA biosynthesis initiating protein (dnaA), ATP operon  
(atpCDGAHFEB), and putative chromosome replication protein (gidA) genes,  
complete cds; and termination factor Rho (rho) gene, partial cds.//0.00  
088:690:57//AF008210

F-HEMBB1001102//Homo sapiens huntingtin interacting protein HYPH mRNA, partial  
cds.//2.1e-76:368:99//AF049612

F-HEMBB1001105//CIT-HSP-2185N1.TR CIT-HSP Homo sapiens genomic clone 218  
5N1, genomic survey sequence.//1.0e-09:136:76//AQ002987

F-HEMBB1001112//Rattus rattus sec61 homologue mRNA, complete cds.//1.0e-108:909:76//M96630

F-HEMBB1001114//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete  
sequence.//7.2e-07:459:59//AC005284

F-HEMBB1001117//HS\_2178\_B1\_E12\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2178 Col=23 Row=J, genomic survey

sequence.//7.8e-50:331:86//AQ068244

F-HEMBB1001119//Human collagen type XII alpha-1 precursor (COL12A1) mRNA  
, complete cds.//1.6e-25:150:98//U73778

F-HEMBB1001126

F-HEMBB1001133//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome System  
s Human BAC library) complete sequence.//2.8e-24:228:80//AC004673

F-HEMBB1001137

F-HEMBB1001142//Homo sapiens chromosome Y, clone 264,M,20, complete sequ  
ence.//1.0e-40:231:76//AC004617

F-HEMBB1001151//Rattus norvegicus golgi peripheral membrane protein p65  
(GRASP65) mRNA, complete cds.//2.9e-47:640:67//AF015264

F-HEMBB1001153//CIT-HSP-2359K11.TR CIT-HSP Homo sapiens genomic clone 23  
59K11, genomic survey sequence.//0.76:136:67//AQ075724

F-HEMBB1001169//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq2  
6.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2),  
ESTs and CA repeat.//9.9e-63:259:79//AL008712

F-HEMBB1001175//Human mRNA for ankyrin motif, complete cds.//2.2e-34:509  
:66//D78334

F-HEMBB1001177//CIT-HSP-2321I17.TR CIT-HSP Homo sapiens genomic clone 23  
21I17, genomic survey sequence.//5.9e-27:320:75//AQ036473

F-HEMBB1001182//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-1  
1-30J5, genomic survey sequence.//5.7e-06:62:96//B85188

F-HEMBB1001199

F-HEMBB1001208//HS\_2026\_B1\_C07\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2026 Col=13 Row=F, genomic survey  
sequence.//0.00018:134:70//AQ229237

F-HEMBB1001209//CITBI-E1-2521F23.TF CITBI-E1 Homo sapiens genomic clone  
2521F23, genomic survey sequence.//1.4e-95:464:98//AQ278357

F-HEMBB1001210//HS\_3102\_A2\_F09\_MF CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=3102 Col=18 Row=K, genomic survey sequence.//2.6e-90:446:98//AQ119196

F-HEMBB1001218//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//1.0e-31:315:72//AL031291

F-HEMBB1001221//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.7e-17:770:59//AC005504

F-HEMBB1001234//H.sapiens CpG island DNA genomic Mse1 fragment, clone 39 f9, forward read cpg39f9.ft1e.//4.0e-30:171:97//Z65435

F-HEMBB1001242//Homo sapiens mRNA for LAK-1, complete cds.//3.8e-30:458:67//AB005754

F-HEMBB1001249//CIT-HSP-2375N19.TF CIT-HSP Homo sapiens genomic clone 23 75N19, genomic survey sequence.//0.0076:250:63//AQ109087

F-HEMBB1001253//Homo sapiens genomic DNA, chromosome 21q11.1, segment 3/28, WORKING DRAFT SEQUENCE.//0.0097:89:80//AP000032

F-HEMBB1001254//CIT-HSP-2320E5.TF CIT-HSP Homo sapiens genomic clone 232 0E5, genomic survey sequence.//3.7e-54:284:97//AQ037173

F-HEMBB1001267//Homo sapiens chromosome 17, clone hRPK.488\_L\_1, complete sequence.//3.5e-30:236:78//AC005303

F-HEMBB1001271//HS\_3011\_A1\_G02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3011 Col=3 Row=M, genomic survey sequence.//5.2e-07:364:62//AQ214217

F-HEMBB1001282//CIT-HSP-2356J20.TF CIT-HSP Homo sapiens genomic clone 23 56J20, genomic survey sequence.//1.8e-16:109:97//AQ060969

F-HEMBB1001288//R.norvegicus mRNA for gephyrin.//3.4e-18:194:77//X66366

F-HEMBB1001289//Genomic sequence from Human 9q34, complete sequence.//4.8e-66:434:74//AC000387

F-HEMBB1001294//HS\_3039\_B1\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey s

quence.//2.0e-90:437:99//AQ155035

F-HEMBB1001302

F-HEMBB1001304//CIT-HSP-2053E15.TF CIT-HSP Homo sapiens genomic clone 20  
53E15, genomic survey sequence.//2.2e-07:370:61//B69144

F-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-  
3) mRNA, complete cds.//5.7e-116:663:85//U92703

F-HEMBB1001315//Homo sapiens chromosome 10 clone LA10NC01\_40\_G\_3 map 10q  
26.1-10q26.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.5e-33:328:77/  
/AC006096

F-HEMBB1001317//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Hu  
man BAC Library) complete sequence.//1.4e-122:680:91//AC006210

F-HEMBB1001326//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete  
sequence.//2.8e-09:518:60//AC004129

F-HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, co  
mplete cds, strain:BALB/c.//3.7e-56:458:79//D63850

F-HEMBB1001335//HS\_3055\_A1\_H10\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3055 Col=19 Row=0, genomic survey  
sequence.//1.0:222:63//AQ147384

F-HEMBB1001337//Human PAC clone DJ0093I03 from Xq23, complete sequence./  
/1.0e-74:319:85//AC003983

F-HEMBB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region  
.//4.0e-135:856:87//U85056

F-HEMBB1001346//Human familial Alzheimer's disease (STM2) gene, complete  
cds.//3.3e-44:481:74//U50871

F-HEMBB1001348//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete  
sequence.//1.8e-17:210:73//AC006041

F-HEMBB1001356//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 u  
nordered pieces.//1.0:386:59//AC005079

F-HEMBB1001364//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complet

e sequence.//0.97:349:61//AC004662

F-HEMBB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p  
11.2-10p12.1, complete sequence.//5.5e-161:766:98//AC005876

F-HEMBB1001367//Homo sapiens chromosome 17, clone hRPC.906\_A\_24, complete  
sequence.//3.0e-55:510:76//AC004408

F-HEMBB1001369//Homo sapiens BAC clone RG163K11 from 7q31, complete sequence.  
//0.048:244:64//AC005192

F-HEMBB1001380//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete  
sequence.//2.5e-26:257:78//AC006204

F-HEMBB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete  
cds.//5.1e-99:571:89//AF071314

F-HEMBB1001387//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene.  
//7.1e-05:546:58//X02354

F-HEMBB1001394//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete  
sequence.//4.0e-129:788:88//AC005023

F-HEMBB1001410//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2  
(RFC2) genes, complete cds.//4.8e-11:632:59//AF045555

F-HEMBB1001424//Mus musculus Chromosome 4 BAC clone BacB6, complete sequence.  
//0.0012:435:59//AC003019

F-HEMBB1001426//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//3.8e-17:360:64//AC005482

F-HEMBB1001429//leucine aminopeptidase [cattle, kidney, mRNA, 2056 nt].  
//4.1e-114:668:88//S65367

F-HEMBB1001436//Homo sapiens FUT2 gene, intron 1, complete sequence.//2.  
3e-37:438:74//AB000931

F-HEMBB1001443//Bos taurus pyruvate dehydrogenase phosphatase mRNA, complete  
cds.//9.1e-92:550:88//L18966

F-HEMBB1001449//Homo sapiens chromosome 5, PAC clone 228g9 (LBNL H142),  
complete sequence.//0.00024:385:62//AC004768

F-HEMBB1001454//Homo sapiens chromosome 19, cosmid R34169, complete sequence.//0.84:577:57//AC005790

F-HEMBB1001458//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//8.0e-40:377:78//AC000382

F-HEMBB1001463//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.011:482:59//AF001549

F-HEMBB1001464//Human chromosome 16p13 BAC clone CIT987SK-3H8 complete sequence.//0.019:263:61//U91320

F-HEMBB1001482//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//1.0e-30:521:66//U92564

F-HEMBB1001500//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-31:479:71//AC004873

F-HEMBB1001521//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.7e-51:680:70//AC005080

F-HEMBB1001527

F-HEMBB1001531//Homo sapiens Chromosome 22q11.2 Cosmid Clone 89h In DGCR Region, complete sequence.//1.3e-79:696:79//AC000089

F-HEMBB1001535//Oaries DNA for polymorphic marker 'OVINRA01' (339 bp).//0.00034:217:62//X89268

F-HEMBB1001536//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//0.54:266:60//AC004548

F-HEMBB1001537//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//4.6e-25:784:61//AC004262

F-HEMBB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//6.9e-50:213:80//AC004605

F-HEMBB1001562//Homo sapiens clone NH0523H20, complete sequence.//0.46:269:60//AC005041

F-HEMBB1001564//Human DNA sequence from clone 192P9 on chromosome Xp11.2

3-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//1.7e-107:620:83//AL020989

F-HEMBB1001565//*Homo sapiens* BAC clone RG437L15 from 8q21, complete sequence.//2.4e-50:734:67//AC004003

F-HEMBB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.

22-12.2. Contains STSs and GSSs, complete sequence.//1.4e-166:816:97//AL031677

F-HEMBB1001586

F-HEMBB1001588//*Homo sapiens* chromosome 19, CIT-HSP-444n24, complete sequence.//1.6e-21:419:65//AC005261

F-HEMBB1001603

F-HEMBB1001618//*Homo sapiens* DNA sequence from PAC 142L7 on chromosome 6 q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//4.5e-29:422:72//Z9 9289

F-HEMBB1001619//HS\_3079\_B1\_A04\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3079 Col=7 Row=B, genomic survey sequence.//0.0010:77:79//AQ123388

F-HEMBB1001630//*Homo sapiens* clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-12:667:59//AC005089

F-HEMBB1001635//*Plasmodium falciparum* MAL3P7, complete sequence.//3.8e-0 5:475:57//AL034559

F-HEMBB1001637//*Homo sapiens* DNA sequence from PAC 934G17 on chromosome 1p36.21. Contains the alternatively spliced CLCN6 gene for chloride channel proteins CLC-6A (KIAA0046) -B, -C and -D, the alternatively spliced NPPA gene coding for Atrial Natriuretic Factor ANF precursor (Atrial Natriuretic peptide ANP, Prepronatriodilatin), the NPPB gene for Brain Natri

uretic Protein BNP, and a pseudogene similar to SBF1 (and other Myotubularin-related protein genes). Contains ESTs, STSs and the genomic marker D1S2740, complete sequence.//9.2e-13:168:76//AL021155

F-HEMBB1001641//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MP012, complete sequence.//0.00097:721:58//AB006702

F-HEMBB1001653//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//0.15:276:63//AC002038

F-HEMBB1001665//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.43:393:61//L14320

F-HEMBB1001668//F16C15-T7 IGF Arabidopsis thaliana genomic clone F16C15, genomic survey sequence.//0.040:275:60//B12308

F-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//7.2e-171:803:98//AB014546

F-HEMBB1001684//Sequence 1 from patent US 5700927.//7.5e-124:883:81//I86429

F-HEMBB1001685//CIT-HSP-228709.TF CIT-HSP Homo sapiens genomic clone 228709, genomic survey sequence.//2.3e-34:191:97//B99261

F-HEMBB1001695//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LC B-2, SPT-2) pseudogene. Contains ESTs, STSs, GSSs, and a putative CpG island, complete sequence.//0.0091:334:63//AL009178

F-HEMBB1001704//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//1.2e-17:144:87//AL023575

F-HEMBB1001706

F-HEMBB1001707//Guinea pig CD19 mRNA, complete cds.//0.57:232:62//M62543

F-HEMBB1001717//*Saccharomyces cerevisiae* mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes.//1.1e-13:723:58//AJ223323

F-HEMBB1001735//Human PAC clone DJ0596009 from 7p15, complete sequence.//1.3e-36:427:73//AC003074

F-HEMBB1001736//*S.pombe* chromosome II cosmid c4B4.//0.0085:479:57//AL023706

F-HEMBB1001747//*Homo sapiens* PAC clone DJ1002N02 from 7p21-p22, complete sequence.//4.0e-112:532:84//AC005376

F-HEMBB1001749//*Homo sapiens* chromosome 17, clone hRPK.259\_G\_18, complete sequence.//1.3e-98:395:82//AC005829

F-HEMBB1001753//*S.maximus* repeat region, 342bp.//4.2e-11:69:85//Z78099

F-HEMBB1001756//*Homo sapiens* full length insert cDNA clone ZD86A11.//0.0015:302:62//AF088064

F-HEMBB1001760//*P.falciparum* complete gene map of plastid-like DNA (IR-A).//0.011:615:56//X95275

F-HEMBB1001762//CIT-HSP-2290J16.TF CIT-HSP *Homo sapiens* genomic clone 2290J16, genomic survey sequence.//0.84:208:64//AQ005184

F-HEMBB1001785//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//0.0019:469:60//AL031746

F-HEMBB1001797//Human heterogenous nuclear RNA W16W.//0.00012:83:86//X17272

F-HEMBB1001802//*Plasmodium falciparum* MAL3P7, complete sequence.//1.8e-11:538:60//AL034559

F-HEMBB1001812//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING DRAFT SEQUENCE.//1.0e-56:304:84//Z98882

F-HEMBB1001816//*Homo sapiens* chromosome 19, cosmid F24083, complete sequence.//3.6e-75:300:87//AC005204

F-HEMBB1001831//*Homo sapiens* PAM COOH-terminal interactor protein 1 (PCI P1) mRNA, complete cds.//2.3e-162:763:98//AF056209

F-HEMBB1001834//CIT-HSP-2291012.TF CIT-HSP Homo sapiens genomic clone 22  
91012, genomic survey sequence.//7.6e-08:73:94//AQ004168

F-HEMBB1001836//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Canc  
er Institute Human PAC Library) complete sequence.//5.7e-30:297:79//AC00  
4801

F-HEMBB1001839//Human Chromosome X, complete sequence.//0.016:293:63//AC  
004073

F-HEMBB1001850//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomi  
c sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0027:812:58//  
AC005504

F-HEMBB1001863//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DR  
AFT SEQUENCE, 3 unordered pieces.//8.3e-43:520:72//AC004581

F-HEMBB1001867//Human proto-oncogene tyrosine-protein kinase (ABL) gene,  
exon 1a and exons 2-10, complete cds.//1.7e-56:399:86//U07563

F-HEMBB1001868//Rattus norvegicus clone 923 polymeric immunoglobulin rec  
eptor mRNA 3' untranslated region, GA rich region, and microsatellites w  
ith GGA-triplet and GAA-triplet repeats.//6.1e-08:234:67//U01145

F-HEMBB1001869//Homo sapiens full length insert cDNA clone YT86F01.//7.4  
e-87:432:97//AF085974

F-HEMBB1001872

F-HEMBB1001874//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 u  
nordered pieces.//3.4e-14:631:61//AC005000

F-HEMBB1001875//Human DNA sequence from clone J428A131, WORKING DRAFT SE  
QUENCE.//0.93:415:57//Z82209

F-HEMBB1001880//Human genomic DNA sequence from clone 30801 on chromosom  
e Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//1.0e-18:7  
29:60//Z93403

F-HEMBB1001899//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from contig 4-10, complete sequence.//0.0038:425:58//AL010216

F-HEMBB1001905//*S.pombe* chromosome III cosmid c330.//1.1e-23:520:62//AL0

31603

F-HEMBB1001906

F-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//3.7e-82:672:81//U47742

F-HEMBB1001910//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0033:566:55//AC005505

F-HEMBB1001911//*Arabidopsis thaliana* chromosome II BAC F26C24 genomic sequence, complete sequence.//1.0:581:58//AC004705

F-HEMBB1001915//*Caenorhabditis elegans* cosmid T05H10, complete sequence.//1.2e-16:283:67//Z47812

F-HEMBB1001921//*Homo sapiens* chromosome 17, clone hCIT.123\_J\_14, complete sequence.//3.4e-07:803:58//AC003950

F-HEMBB1001922//*Plasmodium falciparum* chromosome 2, section 28 of 73 of the complete sequence.//5.0e-06:756:56//AE001391

F-HEMBB1001925//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat, .//3.1e-45:60 9:73//AL009181

F-HEMBB1001930//*Homo sapiens* genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 10/11 .//3.2e-158:745:99//AB020867

F-HEMBB1001944//, complete sequence.//4.1e-60:638:73//AC005815

F-HEMBB1001945//HS\_3185\_B1\_G05\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3185 Col=9 Row=N, genomic survey sequence.//1.0:280:58//AQ188882

F-HEMBB1001947//Human mRNA for KIAA0392 gene, partial cds.//5.6e-20:338:66//AB002390

F-HEMBB1001950//Human lipocortin (LIP) 2 gene, upstream region.//0.0094:

180:63//M62899

F-HEMBB1001952//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 101A4, WORKING DRAFT SEQUENCE.//5.4e-19:329:70//Z93341

F-HEMBB1001953//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence.//0.11:589:58//AC005284

F-HEMBB1001957//Human DNA sequence from PAC 204E5 on chromosome 12. Contains exon similar to Wilms' Tumour-related protein QM-like P2X-like receptor, ATP ligand gated ion channel, ESTs, CpG island.//9.8e-25:446:67//Z98941

F-HEMBB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence.//2.8e-147:727:97//AC005736

F-HEMBB1001967//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//3.2e-56:650:71//AC004963

F-HEMBB1001973//Homo sapiens chromosome 12p13.3 clone RPCI11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//1.2e-42:327:84//AC005844

F-HEMBB1001983//CIT-HSP-2315M4.TF CIT-HSP Homo sapiens genomic clone 2315M4, genomic survey sequence.//8.8e-35:198:96//AQ028071

F-HEMBB1001988//D.polychroa microsatellite sequence (clone Dp 1C e12).//4.5e-07:337:62//X92189

F-HEMBB1001990//HS\_3234\_A1\_G08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234 Col=15 Row=M, genomic survey sequence.//0.039:279:59//AQ204689

F-HEMBB1001996//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE.//0.18:392:58//AL024507

F-HEMBB1001997//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.3e-43:446:71//AC005069

F-HEMBB1002002//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.077:444:58//AC004153

F-HEMBB1002005//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 963K23, WORKING DRAFT SEQUENCE.//3.4e-16:173:78//AL031685

F-HEMBB1002009//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00033:790:56//AC005506

F-HEMBB1002015//Homo sapiens genomic DNA, chromosome 21q11.1, segment 27/28, WORKING DRAFT SEQUENCE.//6.7e-05:126:76//AP000056

F-HEMBB1002042//Oncorhynchus mykiss cytochrome P450 (CYP4V1) mRNA, partial cds.//6.4e-33:402:69//AF046012

F-HEMBB1002043

F-HEMBB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//3.0e-167:809:97//AC005740

F-HEMBB1002045

F-HEMBB1002049//Homo sapiens chromosome 17, clone hRPC.161\_P\_9, complete sequence.//0.87:177:65//AC006237

F-HEMBB1002050//Streptomyces coelicolor cosmid D78.//8.5e-08:644:58//AL034355

F-HEMBB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds.//2.5e-05:402:61//AB014512

F-HEMBB1002069

F-HEMBB1002092//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.8e-104:550:83//AC004064

F-HEMBB1002094//Homo sapiens genomic DNA, 21q region, clone: 125H6N2, genomic survey sequence.//2.9e-49:302:83//AG001476

F-HEMBB1002115//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence.//0.00023:542:61//AC004035

F-HEMBB1002134//Human h-neuro-d4 protein mRNA, complete cds.//7.3e-43:533:70//U43843

F-HEMBB1002139//HS-1048-A2-B02-MR.abi CIT Human Genomic Sperm Library C  
Homo sapiens genomic clone Plate=CT 831 Col=4 Row=C, genomic survey sequence.//0.055:228:66//B38714

F-HEMBB1002142//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from MAL1P5, WORKING DRAFT SEQUENCE.//0.0095:276:64//AL031748

F-HEMBB1002152//Human Chromosome X, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.055:520:57//AC002421

F-HEMBB1002189//Homo sapiens cosmid ICRFc104I0935Q8 from Xq28, complete sequence.//2.6e-05:311:63//AF002998

● F-HEMBB1002190//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.4e-05:647:59//AC005140

F-HEMBB1002193//Sequence 5 from patent US 5709858.//1.8e-34:179:100//I80 846

F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10.//1.2e-23:4 05:67//X52332

● F-HEMBB1002218//HS\_2056\_B1\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=17 Row=F, genomic survey sequence.//3.3e-45:245:97//AQ244711

● F-HEMBB1002232//Human chromosome 11 72g7 cosmid, complete sequence.//1.9 e-21:314:70//U73648

F-HEMBB1002247

F-HEMBB1002249//Homo sapiens DNA sequence from BAC 34I8 on chromosome 6p 21.3-22.1. Contains ZNF184 gene coding for Kruppel related Zinc Finger protein 184, a hnRNP core protein A1 (mouse Fli-2, rat helix destabilizing protein, mouse Topoisomerase-inhibitor suppressed gene TIS) LIKE pseudogene, a HB15 (CD83 antigen precursor) LIKE pseudogene, Ser-tRNA, Glu-tRNA and Met-tRNA (Met-tRNA-i gene 1) genes. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-45:327:83//AL021918

F-HEMBB1002254//Human chromosome 16 BAC clone LANL cosmid-440E5, WORKING  
DRAFT SEQUENCE, 2 unordered pieces.//9.8e-40:315:82//AC002506

F-HEMBB1002255//Plasmodium falciparum MAL3P3, complete sequence.//0.0035  
:312:62//Z98547

F-HEMBB1002266//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic  
sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:469:59//A  
C005504

F-HEMBB1002280//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10,  
complete sequence.//5.3e-18:527:61//AC004682

F-HEMBB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.  
//8.6e-139:818:88//U73642

F-HEMBB1002306//HS\_3109\_A2\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=2 Row=0, genomic survey sequence.//1.3e-75:371:98//AQ148164

F-HEMBB1002327//HS\_3235\_B2\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=20 Row=N, genomic survey sequence.//3.3e-83:418:97//AQ209752

F-HEMBB1002329//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2  
503J7, genomic survey sequence.//3.3e-31:220:88//AQ263402

F-HEMBB1002340

F-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.  
//4.1e-154:724:98//AJ010841

F-HEMBB1002358//Human thymidylate kinase (CDC8) mRNA, complete cds.//3.3  
e-36:192:98//L16991

F-HEMBB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds.//  
1.8e-13:96:96//U55766

F-HEMBB1002364//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 376D21, WORKING DRAFT SEQUENCE.//7.5e-24:202:71//Z98946

F-HEMBB1002371//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic

sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.9e-06:674:56//

AC004153

F-HEMBB1002381//Homo sapiens chromosome 16, cosmid clone RT163 (LANL), complete sequence.//0.34:238:61//AC005222

F-HEMBB1002383

F-HEMBB1002387//CIT-HSP-2173E20.TR CIT-HSP Homo sapiens genomic clone 21 73E20, genomic survey sequence.//5.2e-17:434:66//B91052

F-HEMBB1002409//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-56:324:88//AL008712

F-HEMBB1002415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 364I1, WORKING DRAFT SEQUENCE.//8.9e-35:334:75//AL031319

F-HEMBB1002425//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//1.0e-36:317:76//U62317

F-HEMBB1002442//Rattus norvegicus lin-10 protein homolog (lin-10) mRNA, complete cds.//4.3e-88:296:92//U92010

F-HEMBB1002453//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 86D1, WORKING DRAFT SEQUENCE.//2.7e-43:419:78//AL034349

F-HEMBB1002457//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.3e-27:542:68//AC005534

F-HEMBB1002458//HS\_3246\_A2\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=10 Row=M, genomic survey sequence.//3.2e-51:257:99//AQ217993

F-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//1.9e-87:493:92//U43885

F-HEMBB1002489

F-HEMBB1002492//Arabidopsis thaliana BAC T15B16.//0.028:516:57//AF104919

F-HEMBB1002495//Homo sapiens chromosome 17, clone hRPK.421\_E\_14, complete sequence.//1.1e-16:297:68//AC006141

F-HEMBB1002502//Homo sapiens clone DJ1163L11, complete sequence.//1.1e-9  
1:675:82//AC005230

F-HEMBB1002509//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, c  
omplete sequence.//2.7e-11:648:60//AC004605

F-HEMBB1002510//HS\_3236\_B1\_H11\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3236 Col=21 Row=P, genomic survey  
sequence.//1.2e-06:67:94//AQ205992

F-HEMBB1002520//Homo sapiens BAC clone NH0004N07 from Y, complete sequen  
ce.//1.2e-70:580:72//AC006152

● F-HEMBB1002522//Homo sapiens Xp22 bin 150 clone GSHB-223P11 (Genome Syst  
ems Human BAC library) complete sequence.//5.6e-22:516:64//AC004553

F-HEMBB1002531

F-HEMBB1002534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 668J24, WORKING DRAFT SEQUENCE.//6.9e-62:265:87//AL034346

F-HEMBB1002545//Human BAC clone RG128M16 from 7q21-7q22, complete sequen  
ce.//2.7e-44:200:82//AC000059

F-HEMBB1002550//Homo sapiens PAC clone DJ0910I17 from 7q11.21-q11.23, co  
mplete sequence.//0.22:161:68//AC004927

● F-HEMBB1002556//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete  
sequence.//7.5e-43:306:77//AC004861

F-HEMBB1002579

F-HEMBB1002582//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 349A12, WORKING DRAFT SEQUENCE.//0.00018:431:61//AL033520

F-HEMBB1002590//Yeast (S.cerevisiae) mitochondrial apocytochrome b gene,  
3' flank.//0.78:147:64//J01471

F-HEMBB1002596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 9E21, WORKING DRAFT SEQUENCE.//3.6e-50:692:69//AL008639

F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//9.1e-1  
51:710:98//AF089749

F-HEMBB1002601//Human BAC clone RG020D02 from 7q22, complete sequence.//

1.5e-07:416:60//AC002381

F-HEMBB1002603//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//0.40:341:60//AC002454

F-HEMBB1002607//Mus musculus homeobox containing nuclear transcriptional factor Hmx1 (Hmx1) gene, complete cds.//0.0042:460:60//AF009614

F-HEMBB1002610//Homo sapiens Chromosome 12q24 PAC RPCI3-462E2 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.3e-23:559:63//AC003029

● F-HEMBB1002613//Homo sapiens Chromosome 22q12 BAC Clone 566c1, complete sequence.//4.2e-17:441:63//AC000025

F-HEMBB1002614//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//0.013:324:56//AE001417

F-HEMBB1002617//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//2.1e-07:441:60//AF001550

F-HEMBB1002623//C.hyalina microsatellite marker DNA (id ATCC4).//0.57:106:66//Z95304

F-HEMBB1002635//Human JNK3 alpha2 protein kinase (JNK3A2) mRNA, complete cds.//4.8e-22:127:100//U34819

● F-HEMBB1002664//HS\_2265\_A1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2265 Col=11 Row=0, genomic survey sequence.//0.54:115:67//AQ101557

F-HEMBB1002677//Homo sapiens (subclone 3\_d1 from P1 H25) DNA sequence, complete sequence.//2.2e-49:784:68//L81774

F-HEMBB1002683//Homo sapiens type IV collagen 5a chain (COL4A5) gene, exon 23.//1.0:112:63//U04492

F-HEMBB1002684//HS-1050-A2-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 772 Col=12 Row=M, genomic survey sequence.//4.4e-07:86:84//B39748

F-HEMBB1002686//HS-1023-B2-F10-MR.abi CIT Human Genomic Sperm Library C

Homo sapiens genomic clone Plate=CT 802 Col=20 Row=L, genomic survey sequence.//0.98:183:61//B34077

F-HEMBB1002692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108H3, WORKING DRAFT SEQUENCE.//0.00039:408:60//AL033525

F-HEMBB1002697//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.3e-35:323:74//AC004955

F-HEMBB1002699//Mus musculus D6MM5e protein (D6Mm5e) and DOK protein (Dok) genes, complete cds; and LOR2 protein (Lor2) gene, partial cds.//0.031:325:62//AF084363

F-HEMBB1002702//HS-1025-A2-D01-MR.abi CIT Human Genomic Sperm Library C  
Homo sapiens genomic clone Plate=CT 804 Col=2 Row=G, genomic survey sequence.//1.8e-25:158:95//B34720

F-HEMBB1002705//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds).//1.7e-137:534:96//AB003151

F-HEMBB1002712//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS.//0.0019:612:58//Z71187

F-MAMMA1000009//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//6.1e-43:354:81//AC003117

F-MAMMA1000019

F-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FM 05).//2.0e-40:185:97//Z47553

F-MAMMA1000025//Homo sapiens PAC clone DJ0806A17 from 7p13-p14, complete sequence.//1.0:211:65//AC005483

F-MAMMA1000043//Human angiotensin I-converting enzyme (ACE) gene, intron 12.//0.075:204:65//M73275

F-MAMMA1000045//Human DNA sequence from clone 142F18 on chromosome Xq26.

3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence.//4.1e-122:495:79//AL031073

F-MAMMA1000055//*M.musculus* mRNA for testin.//2.1e-35:559:66//X78989

F-MAMMA1000057//*Homo sapiens* chromosome 17, clone hRPK.259\_G\_18, complete sequence.//5.5e-121:703:89//AC005829

F-MAMMA1000069//*Homo sapiens* minisatellite ceb1 repeat region.//0.00013:329:60//AF048727

F-MAMMA1000084//*Homo sapiens* DNA sequence from PAC 958B3 on chromosome X p22.11-Xp22.22. Contains ESTs STS and CpG island.//2.1e-53:445:79//Z93023

F-MAMMA1000085//*Caenorhabditis elegans* cosmid Y23H5A.//0.0017:164:64//AF077541

F-MAMMA1000092//*Homo sapiens* BAC clone GS465N13 from 7p15-p21, complete sequence.//1.2e-70:598:78//AC004744

F-MAMMA1000103//*Homo sapiens* chromosome 17, clone hCIT.91\_J\_4, complete sequence.//1.1e-156:857:92//AC003976

F-MAMMA1000117//HS\_3223\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3223 Col=16 Row=H, genomic survey sequence.//5.4e-100:527:94//AQ221160

F-MAMMA1000129//ryanodine receptor.//0.055:492:59//A20359

F-MAMMA1000133

F-MAMMA1000134//HS\_3078\_B1\_C02\_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//2.1e-93:462:97//AQ144362

F-MAMMA1000139//*Homo sapiens* Xp22 PAC RPCI1-5G11 (from Roswell Park Cancer Center) complete sequence.//3.3e-14:322:65//AC002369

F-MAMMA1000143//*Homo sapiens* mRNA for KIAA0685 protein, complete cds.//6.9e-25:148:97//AB014585

F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2)

mRNA, complete cds.//1.0e-29:219:87//AF031924

F-MAMMA1000163

F-MAMMA1000171//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//6.3e-14:92:88//AC005393

F-MAMMA1000173//Mus musculus SH3-containing protein SH3P7 mRNA, complete cds. similar to Human Drebrin.//2.2e-114:698:87//U58884

F-MAMMA1000175//HS\_3050\_B1\_B03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=5 Row=D, genomic survey sequence.//6.2e-73:357:99//AQ102678

F-MAMMA1000183//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//4.6e-94:904:73//AL023808

F-MAMMA1000198//Z.diploperennis repetitive DNA (clone ZEAR 266).//0.18:1 52:70//X53610

F-MAMMA1000221//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.017:99:75//AC004583

F-MAMMA1000227//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467K16, WORKING DRAFT SEQUENCE.//0.36:312:62//AL031283

F-MAMMA1000241//HS\_3217\_B1\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3217 Col=3 Row=D, genomic survey sequence.//1.9e-94:456:98//AQ193401

F-MAMMA1000251//Homo sapiens NF2 gene.//0.00092:270:64//Y18000

F-MAMMA1000254//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0034:777:57//AC005140

F-MAMMA1000257//Homo sapiens DNA sequence from PAC 201D7 on chromosome 6 p22.1-22.3. Contains EST and STS.//0.00036:230:65//AL022717

F-MAMMA1000264//Homo sapiens (subclone 9\_f5 from P1 H17) DNA sequence, complete sequence.//1.5e-30:499:68//L81612

F-MAMMA1000266//Bacillus lycneorum strain pMEL12 Bag320 satellite DNA.//

0.28:218:64//AF034430

F-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//1.4e-157:788:96//AF001549

F-MAMMA1000277//Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.//0.70:320:61//AL021897

F-MAMMA1000278//Sequence 23 from patent US 5708157.//9.3e-103:540:95//I8 0055

F-MAMMA1000279//Human DNA sequence from clone 769D20 on chromosome Xp21.

● 1-21.3 Contains EST, STS, GSS, complete sequence.//2.4e-49:262:77//AL031 643

F-MAMMA1000284//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence.//1.1e-30:324:75//B03004

F-MAMMA1000287//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//2.7 e-54:401:83//AC006213

F-MAMMA1000302//Drosophila melanogaster complete mitochondrial genome.//0.0051:307:61//U37541

● F-MAMMA1000307//Homo sapiens chromosome 12p13.3 clone RPCI5-1154L15, WORKING DRAFT SEQUENCE, 67 unordered pieces.//0.15:449:59//AC006205

F-MAMMA1000309//cDNA coding human apolipoprotein E3.//0.00010:691:58//E0 0359

F-MAMMA1000312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 798A17, WORKING DRAFT SEQUENCE.//0.27:301:60//AL031274

F-MAMMA1000313

F-MAMMA1000331//Human Chromosome 16 BAC clone CIT987SK-A-735G6, complete sequence.//9.8e-06:151:71//AC002400

F-MAMMA1000339

F-MAMMA1000340//HS\_2181\_B2\_F07\_MR CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=2181 Col=14 Row=L, genomic survey sequence.//4.3e-05:181:68//AQ024288

F-MAMMA1000348//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence.//5.3e-30:575:66//AC004139

F-MAMMA1000356//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-52:264:76//AC005052

F-MAMMA1000360//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.//6.5e-91:569:88//AC004879

F-MAMMA1000361//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//1.4e-42:315:83//Z98950

F-MAMMA1000372//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//2.9e-114:516:89//AL022345

F-MAMMA1000385//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence.//6.9e-26:377:71//AQ279944

F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//3.7e-148:710:98//AB015132

F-MAMMA1000395

F-MAMMA1000402//Homo sapiens clone DJ0718N17, complete sequence.//4.0e-15:845:85//AC005999

F-MAMMA1000410//HS\_3245\_A1\_C02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=3 Row=E, genomic survey sequence.//9.6e-42:350:80//AQ205768

F-MAMMA1000413//HS\_3223\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=2 Row=L, genomic survey sequence.//1.6e-48:318:89//AQ188456

F-MAMMA1000414//HS\_2027\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=8 Row=F, genomic survey sequence.//1.4e-46:286:92//AQ231369

F-MAMMA1000416//*Drosophila melanogaster* DNA sequence (P1s DS07528 (D169)  
and DS06665 (D220)), complete sequence.//9.4e-33:310:72//AC004640

F-MAMMA1000421//*Homo sapiens* clone DJ1129D05, complete sequence.//3.3e-2  
9:223:84//AC005630

F-MAMMA1000422

F-MAMMA1000423//*Drosophila yakuba* mitochondrial DNA molecule.//2.2e-10:6  
39:57//X03240

F-MAMMA1000424//*Homo sapiens* DNA from chromosome 19, BAC 33152, complete  
sequence.//4.6e-47:556:68//AC003973

● F-MAMMA1000429//*Mus musculus* SDP8 mRNA, complete cds.//8.0e-99:545:92//A  
F062484

F-MAMMA1000431//*Homo sapiens* clone DJ1039L24, WORKING DRAFT SEQUENCE, 3  
unordered pieces.//4.8e-41:289:79//AC005283

F-MAMMA1000444//Human DNA sequence from clone 714B7 on chromosome 22q12.  
2-13.2 Contains CYTOCHROME C OXIDASE VIIB precursor like pseudogene and  
ESTs, complete sequence.//2.3e-34:291:80//Z99755

F-MAMMA1000446

F-MAMMA1000458//*Mus musculus* clone OST9003, genomic survey sequence.//5.  
0e-53:231:84//AF046620

● F-MAMMA1000468//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 291J10, WORKING DRAFT SEQUENCE.//0.75:303:60//Z93017

F-MAMMA1000472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 414D7, WORKING DRAFT SEQUENCE.//4.0e-41:403:77//AL033543

F-MAMMA1000478//*Homo sapiens* clone RG270D13, WORKING DRAFT SEQUENCE, 18  
unordered pieces.//9.5e-54:369:77//AC005081

F-MAMMA1000483//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-44M2, comp  
lete sequence.//3.6e-34:332:77//AC004381

F-MAMMA1000490//*Homo sapiens* 12q13.1 PAC RPCI1-90J4 (Roswell Park Cancer  
Institute Human PAC library) complete sequence.//8.9e-128:822:87//AC003

686

F-MAMMA1000500//CIT-HSP-231905.TF CIT-HSP Homo sapiens genomic clone 231  
905, genomic survey sequence.//4.8e-29:175:94//AQ044812

F-MAMMA1000501//Homo sapiens DNA sequence from clone 78F24 on chromosome  
22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP)  
LIKE gene. Contains GSSs and an STS, complete sequence.//5.7e-45:334:82/  
/AL022336

F-MAMMA1000516//Human DNA sequence from PAC 50A13 on chromosome Xp11. Co  
ntains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1,  
ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA  
repeat.//2.9e-43:529:69//Z92545

F-MAMMA1000522//Human DNA sequence from clone 20J23 on chromosome Xq26.2  
-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ra  
s-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.  
//2.0e-14:380:63//AL022576

F-MAMMA1000524//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p  
11.2-10p12.1, complete sequence.//1.4e-22:420:66//AC006101

F-MAMMA1000559//Human HepG2 3' region cDNA, clone hmd3f08.//5.4e-29:168:  
97//D16922

F-MAMMA1000565//RPCI11-61K6.TJ RPCI11 Homo sapiens genomic clone R-61K6,  
genomic survey sequence.//1.7e-120:561:100//AQ194238

F-MAMMA1000567//Human DNA sequence from PAC 179D3, between markers DXS67  
91 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs an  
d CpG island.//3.1e-43:387:80//Z81370

F-MAMMA1000576//Homo sapiens BAC clone RG442F18 from 2, complete sequenc  
e.//1.2e-30:237:75//AC005104

F-MAMMA1000583//RPCI11-60M22.TJ RPCI11 Homo sapiens genomic clone R-60M2  
2, genomic survey sequence.//9.6e-102:487:99//AQ198091

F-MAMMA1000585//Homo sapiens clone UWGC:djs14 from 7p14-15, complete seq

uence.//5.2e-39:370:78//AC006195

F-MAMMA1000594//Homo sapiens chromosome 19, cosmid R31646, complete sequence.//3.9e-43:328:83//AC005338

F-MAMMA1000597//Homo sapiens chromosome 17, clone hRPK.481\_C\_4, complete sequence.//1.5e-32:259:82//AC005839

F-MAMMA1000605//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.4e-59:318:83//AL031297

F-MAMMA1000612//HS\_2188\_A2\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//4.8e-30:171:96//AQ116793

F-MAMMA1000616//HS\_3176\_A1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3176 Col=11 Row=I, genomic survey sequence.//4.7e-28:287:79//AQ300310

F-MAMMA1000621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 273F20, WORKING DRAFT SEQUENCE.//0.015:478:58//AL034371

F-MAMMA1000623

F-MAMMA1000625//DNA encoding Hepatitis C virus antigen.//0.93:196:61//E06898

F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds.//0.95:365:59//AF023674

F-MAMMA1000664//HS\_3096\_B1\_C02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3096 Col=3 Row=F, genomic survey sequence.//2.7e-51:257:99//AQ145137

F-MAMMA1000669//Homo sapiens chromosome 19, cosmid R26908, complete sequence.//2.0e-66:586:67//AC004785

F-MAMMA1000670//HS\_2243\_B2\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2243 Col=16 Row=B, genomic survey sequence.//8.7e-05:94:80//AQ153650

F-MAMMA1000672//Mus musculus clone OST8270, genomic survey sequence.//3.

9e-64:471:81//AF046705

F-MAMMA1000684//Suid herpesvirus 1 Rsp40 mRNA, partial cds.//1.2e-07:186  
:67//U27489

F-MAMMA1000696//Human oligodendrocyte myelin glycoprotein (OMG) exons 1-  
2; neurofibromatosis 1 (NF1) exons 28-49; ecotropic viral integration si-  
te 2B (EVI2B) exons 1-2; ecotropic viral integration site 2A (EVI2A) exo-  
ns 1-2; adenylate kinase (AK3) exons 1-2.//3.0e-53:653:70//L05367

F-MAMMA1000707//CIT-HSP-2302019.TR CIT-HSP Homo sapiens genomic clone 23  
02019, genomic survey sequence.//1.8e-08:131:77//AQ017947

● F-MAMMA1000713//Rattus norvegicus clone1 polymeric immunoglobulin recept-  
or mRNA 3' untranslated region, GA rich region, and microsatellites with  
GGA-triplet and GAA-triplet repeats.//0.062:134:67//U00762

F-MAMMA1000714//Chicken hsp90 gene for 90 kDa-heat shock protein 5'-end.  
//1.0:266:61//X15028

F-MAMMA1000718//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 21  
71B10, genomic survey sequence.//3.6e-05:289:60//B95401

F-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequ-  
ence.//4.4e-184:842:98//AC005781

● F-MAMMA1000723//Homo sapiens clone DJ0892G19, complete sequence.//8.8e-0  
5:430:60//AC004917

F-MAMMA1000731//Drosophila melanogaster DNA sequence (P1 DS07049 (D133))  
, complete sequence.//3.8e-55:796:66//AC004274

F-MAMMA1000732//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequ-  
ence, containing ribosomal protein homologue pseudogene L23a.//6.6e-77:5  
55:74//AF064859

F-MAMMA1000733//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from MAL1P6, WORKING DRAFT SEQUENCE.//0.98:479:58//AL031749

F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//7.3e-168  
:802:98//AF100141

F-MAMMA1000738//*S.cerevisiae* chromosome XIV reading frame ORF YNL132w.//

8.6e-31:626:63//Z71408

F-MAMMA1000744//*Gorilla* Alu-repetitive sequence in beta-globin gene cluster.//2.7e-54:410:82//X06123

F-MAMMA1000746//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-A-10F4, complete sequence.//3.7e-109:779:83//AC004158

F-MAMMA1000752//*Homo sapiens* clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.2e-20:444:63//AC005075

F-MAMMA1000760//*Homo sapiens* clone RG015P03, complete sequence.//1.5e-44:403:79//AC005048

F-MAMMA1000761//*Homo sapiens* Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.3e-22:159:81//AC004166

F-MAMMA1000775//*Homo sapiens* chromosome 17, clone hRPK.849\_N\_15, complete sequence.//1.3e-51:789:68//AC005703

F-MAMMA1000776//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//5.7e-40:238:78//Z95116

F-MAMMA1000778//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//7.6e-29:222:84//AL031118

F-MAMMA1000782//Human 2,4-dienoyl-CoA reductase gene, exon 9.//0.90:137:62//U94987

F-MAMMA1000798//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.00058:163:71//AC003656

F-MAMMA1000802//*Homo sapiens* chromosome 19, cosmid R33729, complete sequence.//6.3e-151:714:99//AC005339

F-MAMMA1000824//*Homo sapiens* 12p13.3 BAC RPCI11-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//4.2e-104:503:99//AC

005912

F-MAMMA1000831//Homo sapiens clone UWGC:g1211a139, complete sequence.//0  
.76:302:58//AC005502

F-MAMMA1000839//Human BAC clone RG013L03 from 7q21, complete sequence.//  
1.9e-54:322:68//AC002456

F-MAMMA1000841//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 968D22, WORKING DRAFT SEQUENCE.//6.7e-140:647:92//AL023755

F-MAMMA1000842//, complete sequence.//0.0068:499:59//AC005817

F-MAMMA1000843//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic  
sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.13:439:59//AC0  
04710

F-MAMMA1000845//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from MAL4P1, WORKING DRAFT SEQUENCE.//2.2e-05:208:64//AL034557

F-MAMMA1000851//Gallus domesticus filamin gene 5' region, partial cds.//  
0.86:193:63//U00146

F-MAMMA1000855//Human minisatellite region detected by myoglobin 33-repe  
at probe, clone lambda 33.10.//0.081:229:62//M30549

F-MAMMA1000856//B.taurus microsatellite marker ETH8 (D6S3) DNA.//0.0024:  
253:60//Z22747

F-MAMMA1000859//Sequence 6 from Patent W09722695.//2.3e-79:533:82//A6355

3

F-MAMMA1000862

F-MAMMA1000863//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21  
/28, WORKING DRAFT SEQUENCE.//1.0e-28:439:64//AP000050

F-MAMMA1000865

F-MAMMA1000867//CIT-HSP-2385J8.TR.1 CIT-HSP Homo sapiens genomic clone 2  
385J8, genomic survey sequence.//0.00017:158:70//AQ240906

F-MAMMA1000875//Homo sapiens DNA sequence from PAC 232G24 on chromosome  
Xq27.1-q27.3. Contains two exons similar to MAGE gene family, EST, CA re

peat, STS, complete sequence.//1.0:121:68//AL022152

F-MAMMA1000876//Homo sapiens clone HS19.6 Alu-Ya5 sequence.//8.4e-41:185  
:90//AF015152

F-MAMMA1000877//Homo sapiens DNA sequence from clone 78F24 on chromosome  
22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP)  
LIKE gene. Contains GSSs and an STS, complete sequence.//8.3e-57:522:75/  
/AL022336

F-MAMMA1000880//Homo sapiens full length insert cDNA clone ZD54A10.//5.2  
e-26:143:100//AF086327

● F-MAMMA1000883//Human DNA sequence from clone 786D3 on chromosome 22q13.  
31-33 Contains GSS, complete sequence.//0.99:225:63//AL023801

F-MAMMA1000897//R.norvegicus mRNA for plasma protein.//4.8e-07:479:58//Y  
11283

F-MAMMA1000905//F26L5TRB IGF Arabidopsis thaliana genomic clone F26L5, g  
enomic survey sequence.//0.94:115:66//B61433

F-MAMMA1000906//HS\_3110\_B2\_A11\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3110 Col=22 Row=B, genomic survey  
sequence.//2.5e-63:548:78//AQ182819

● F-MAMMA1000908//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 27K12, WORKING DRAFT SEQUENCE.//5.2e-80:480:90//AL033397

F-MAMMA1000914//Plasmodium falciparum MAL3P8, complete sequence.//7.6e-0  
9:596:58//AL034560

F-MAMMA1000921//CIT-HSP-2171D8.TR CIT-HSP Homo sapiens genomic clone 217  
1D8, genomic survey sequence.//6.6e-07:249:66//B89575

F-MAMMA1000931//Homo sapiens clone DJ0892G19, complete sequence.//2.9e-4  
3:415:66//AC004917

F-MAMMA1000940//HS-1056-A2-E02-MF.abi CIT Human Genomic Sperm Library C  
Homo sapiens genomic clone Plate=CT 778 Col=4 Row=I, genomic survey sequ  
ence.//6.1e-44:235:78//B47296

F-MAMMA1000941//*Homo sapiens* Chromosome 16 BAC clone CIT987-SKA-113A6  
complete genomic sequence, complete sequence.//9.4e-48:443:75//AC002299

F-MAMMA1000942//Human DNA sequence from clone 914P14 on chromosome Xq23  
Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat,  
GSS, complete sequence.//1.8e-14:175:76//AL031117

F-MAMMA1000943//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC492 genomic  
sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0082:684:56//A  
C005308

F-MAMMA1000956//*Homo sapiens* chromosome 16, cosmid clone 363E3 (LANL), c  
omplete sequence.//3.3e-30:530:67//AC004643

F-MAMMA1000957//HS\_3039\_A2\_C08\_MF CIT Approved Human Genomic Sperm Libra  
ry D *Homo sapiens* genomic clone Plate=3039 Col=16 Row=E, genomic survey  
sequence.//1.3e-72:390:94//AQ155121

F-MAMMA1000962//*Homo sapiens* clone DJ0756H11, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//1.8e-58:318:86//AC006001

F-MAMMA1000968//*Homo sapiens* DNA sequence from clone 511B24 on chromosom  
e 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLGG1 gene  
for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC  
3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the  
KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribo  
somal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs  
, STSs and GSSs, complete sequence.//1.4e-18:396:65//AL022394

F-MAMMA1000975//Human DNA sequence from clone 344I7 on chromosome Xp11.2  
1-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8,  
KRT8) pseudogene, ESTs and a GSS, complete sequence.//1.4e-79:690:77//A  
L024458

F-MAMMA1000979//*Homo sapiens* PAC clone DJ1186C01 from 7q21.2-q31.1, comp  
lete sequence.//0.089:214:66//AC004991

F-MAMMA1000987//Human PAC clone DJ527C21 from Xq23, complete sequence.//

1.1e-58:458:82//AC000114

F-MAMMA1000998//Human DNA sequence from PAC 997K18 on chromosome 20p12.

Contains ESTs and CA repeat.//1.1e-05:439:62//AL021406

F-MAMMA1001003//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq

21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//0.24:166:68//AL022401

F-MAMMA1001008//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT

SEQUENCE.//1.6e-103:139:99//AJ011929

F-MAMMA1001021//Homo sapiens clone 24544 beta-dystrobrevin mRNA, partial cds.//6.5e-48:465:76//AF070567

F-MAMMA1001024//CITBI-E1-2501L21.TF.1 CITBI-E1 Homo sapiens genomic clone 2501L21, genomic survey sequence.//1.0:175:62//AQ241701

F-MAMMA1001030//Homo sapiens G protein-coupled receptor LGR5 (LGR5) mRNA, complete cds.//1.1e-30:753:61//AF061444

F-MAMMA1001035//Human Chromosome 16 BAC clone CIT987SK-A-1000D7, complete sequence.//7.9e-24:256:76//AC002990

F-MAMMA1001038//CIT-HSP-2284N21.TF CIT-HSP Homo sapiens genomic clone 2284N21, genomic survey sequence.//0.96:78:75//AQ000903

F-MAMMA1001041//Chicken mRNA for alpha-actinin, complete cds.//2.8e-09:355:63//D26597

F-MAMMA1001050//Homo sapiens BAC clone RG060P12 from 7q21, complete sequence.//2.6e-40:378:76//AC002457

F-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//4.8e-97:661:83//L25125

F-MAMMA1001067//Homo sapiens genomic intron breakpoint sequence of MLL rearrangement, 285 bp.//2.8e-18:110:100//AJ000169

F-MAMMA1001073//HS\_3046\_A2\_G08\_MF CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=3046 Col=16 Row=M, genomic survey sequence.//1.0:142:68//AQ098420

F-MAMMA1001074//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//1.2e-23:386:70//AL031733

F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence.//1.1e-27:559:65//L09749

F-MAMMA1001078//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//2.0e-22:384:69//AC006120

F-MAMMA1001080//Human immunoglobulin heavy chain variable region (VH III family) from IgM rheumatoid factor.//6.4e-58:327:92//L29155

F-MAMMA1001082//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//3.8e-87:695:77//AC004087

F-MAMMA1001091//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//7.0e-05:594:60//AC005256

F-MAMMA1001092//Human DNA sequence from PAC 49C23 on chromosome X contains malate dehydrogenase pseudogene and STS.//1.6e-91:174:87//Z93019

F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds.//6.4e-23:507:66//AF016045

F-MAMMA1001110//Homo sapiens chromosome 19, cosmid F16815, complete sequence.//0.77:316:60//AC004637

F-MAMMA1001126//Homo sapiens PAC 50H2 in the CUTL1 locus, complete sequence.//3.3e-21:237:73//AF047825

F-MAMMA1001133//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//0.97:202:63//Z95116

F-MAMMA1001139//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//1.6e-84:406:82//S70011

F-MAMMA1001143//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//1.3e-14:182:76//AL0223

F-MAMMA1001145//Human DNA sequence from cosmid cU115G11, between markers DDX6791 and DDX8038 on chromosome X contains ESTs and STS.//5.2e-87:714:78//Z71187

F-MAMMA1001154//CIT-HSP-2341D13.TF CIT-HSP Homo sapiens genomic clone 23 41D13, genomic survey sequence.//0.00051:249:61//AQ055735

F-MAMMA1001161//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence.//2.2e-30:410:70//AC004518

F-MAMMA1001162//Homo sapiens full length insert cDNA clone ZA79C01.//2.4e-13:87:100//AF086123

F-MAMMA1001181//Mus musculus C2C12 unknown mRNA, partial cds.//9.3e-15:4 32:60//U31629

F-MAMMA1001186//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//6.8e-57:670:72//AC005696

F-MAMMA1001191

F-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//1.5e-117:759:84 //U29156

F-MAMMA1001202

F-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.5e-161:764:98//AC005412

F-MAMMA1001206//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//5.1e-30:535:65//AC004099

F-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//8.4e-182:860:98//AC005393

F-MAMMA1001220//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.7e-58:690:70//AC004875

F-MAMMA1001222//Mouse loricrin mRNA, complete cds.//2.7e-07:624:58//M343  
98

F-MAMMA1001243//Homo sapiens chromosome 17, clone hRPK.192\_H\_23, complete sequence.//0.91:177:66//AC005726

F-MAMMA1001244

F-MAMMA1001249//Human 28S ribosomal RNA psuedogenes and alu repeat region sequence.//6.7e-09:502:58//U67616

F-MAMMA1001256//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//5.0e-37:342:80//Z99495

F-MAMMA1001259

F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds.//8.7e-40:659:64//AB014561

F-MAMMA1001268//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//4.9e-43:265:81//AC004453

F-MAMMA1001271//Salmo salar DNA for a cryptic repeat.//2.6e-06:311:63//AJ012206

F-MAMMA1001274//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.6e-70:327:83//AC004840

F-MAMMA1001280//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-05:276:66//AC003035

F-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//3.6e-98:199:98//AL022314

F-MAMMA1001296//RPCI11-38B4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-38B4, genomic survey sequence.//4.7e-33:292:71//AQ030084

F-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//1.6e-182:860:98//AC005703

F-MAMMA1001305//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Act

ivating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D2 2S1168 and a CA repeat polymorphism, complete sequence.//1.9e-70:163:97//Z93244

F-MAMMA1001322//Human DNA sequence from clone 774I24 on chromosome 1q24. 1-24.3 Contains protein similar to pregnancy-associated plasma protein A precursor neuronal migration protein astrotactin, ESTs, STS and GSS, complete sequence.//2.6e-19:379:68//AL031290

F-MAMMA1001324//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 197L1, WORKING DRAFT SEQUENCE.//4.5e-131:751:90//AL031390

F-MAMMA1001330

F-MAMMA1001341//Sus scrofa.//1.6e-36:420:73//Z46906

F-MAMMA1001343//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//1.1e-05:818:58//AL031744

F-MAMMA1001346

F-MAMMA1001383//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//2.0e-44:505:74//AC004086

F-MAMMA1001388//Human IGF binding protein complex acid-labile subunit mRNA, complete cds.//1.5e-07:415:58//M86826

F-MAMMA1001397//Human DNA sequence from clone 462D8 on chromosome 22q11. 21-12.1 Contains EST, STS and GSS, complete sequence.//1.6e-23:209:75//AL022332

F-MAMMA1001408//HS\_3242\_A1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=21 Row=0, genomic survey sequence.//2.7e-07:181:69//AQ207300

F-MAMMA1001411//Homo sapiens autosomal dominant polycystic kidney disease type II protein (PKD2) gene, exon 14.//0.98:120:68//AF004872

F-MAMMA1001419//HS\_2053\_B1\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=23 Row=L, genomic survey sequence.//1.9e-75:424:93//AQ244585

F-MAMMA1001420//Homo sapiens chromosome 4 clone B203C23 map 4q25, complete sequence.//2.4e-09:199:70//AC004049

F-MAMMA1001435//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-201104, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-42:558:69//AC004529

F-MAMMA1001442//Plasmodium falciparum chromosome 2, section 37 of 73 of the complete sequence.//0.0019:516:56//AE001400

F-MAMMA1001446//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//3.6e-42:486:70//AC003684

F-MAMMA1001452//RPCI11-48022.TJ RPCI11 Homo sapiens genomic clone R-48022, genomic survey sequence.//5.3e-87:423:98//AQ199294

F-MAMMA1001465//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING DRAFT SEQUENCE.//0.00038:114:75//AL033543

F-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//4.1e-99:604:87//L31783

F-MAMMA1001487//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0e-13:158:77//AC005486

F-MAMMA1001501//Human mRNA for calcium activated neutral protease large subunit (muCANP, calpain, EC 3.4.22.17).//9.6e-52:438:81//X04366

F-MAMMA1001502//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B7, WORKING DRAFT SEQUENCE.//3.7e-152:720:99//AL031714

F-MAMMA1001510//Human PAC clone DJ43804 from 22q12.1-qter, complete sequence.//1.1e-05:371:61//AC002378

F-MAMMA1001522

F-MAMMA1001547

F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.3e-128:614:98//AB007931

F-MAMMA1001575//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//0.97:154:68//AF001548

F-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//1.8e-95:529:91/

/M61764

F-MAMMA1001590//Human DNA sequence from clone 125H2 on chromosome 22q11-12 Contains part of myosin heavy chain gene, EST, CA repeat, STS, GSS, complete sequence.//1.8e-07:104:84//Z98949

F-MAMMA1001600//HS\_3022\_A2\_H01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=2 Row=0, genomic survey sequence.//1.6e-66:405:90//AQ163791

F-MAMMA1001604//Human DNA sequence from clone 1114G22 on chromosome 1q24-25 Contains EST, CA repeat, Ninenin like sequence, complete sequence.//0.00043:715:58//AL008626

F-MAMMA1001606//jd114 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 2G6, genomic survey sequence.//0.19:266:62//B13685

F-MAMMA1001620//Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds.//9.7e-54:442:69//AF053630

F-MAMMA1001627//X.borealis ribosomal spacer DNA, with a DNaseI-hypersensitive site.//0.14:221:62//M29833

F-MAMMA1001630//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.0e-47:611:71//AC005412

F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds.//1.1e-42:611:67//U57796

F-MAMMA1001635//Human BAC clone RG072E11 from 7q21-7q22, complete sequence.//4.0e-35:407:70//AC000118

F-MAMMA1001649//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.44:245:63//AL022577

F-MAMMA1001654//Mouse transcriptional control element.//0.0025:189:63//M17284

F-MAMMA1001663//CIT-HSP-2165E16.TR CIT-HSP Homo sapiens genomic clone 21  
65E16, genomic survey sequence.//9.7e-05:146:66//B95491

F-MAMMA1001670//HS\_3136\_A1\_G06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=11 Row=M, genomic survey sequence.//3.1e-28:237:85//AQ148779

F-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//3.3e-181:863:98//AC005614

F-MAMMA1001679//HS\_3054\_A1\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=0, genomic survey sequence.//1.0:89:70//AQ106118

F-MAMMA1001683//Spermatozopsis similis mRNA for 90 kD basal apparatus-protein.//8.3e-07:480:62//AJ224970

F-MAMMA1001686//HS\_3219\_B1\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=5 Row=B, genomic survey sequence.//0.00072:180:65//AQ180345

F-MAMMA1001692//HS\_3047\_B1\_B10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=19 Row=D, genomic survey sequence.//2.5e-94:459:98//AQ134228

F-MAMMA1001711//Homo sapiens clone DJ0635005, WORKING DRAFT SEQUENCE, 7  
unordered pieces.//1.2e-42:316:82//AC004845

F-MAMMA1001715//CIT-HSP-2347A14.TF CIT-HSP Homo sapiens genomic clone 23  
47A14, genomic survey sequence.//1.1e-60:413:87//AQ059125

F-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//1.8e-133:646:97//AF095687

F-MAMMA1001735//chicken brain tubulin beta chain mRNA.//3.5e-110:740:84/  
J00913

F-MAMMA1001740//Human DNA sequence from PAC 136017 on chromosome X contains ESTs and STS.//0.98:416:57//Z72001

F-MAMMA1001743//Homo sapiens clone DJ0981007, complete sequence.//3.2e-1

6:194:75//AC006017

F-MAMMA1001744//Homo sapiens DNA sequence from clone 466I8 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//0.0036:181:66//AL030998

F-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence.//1.2e-60:822:68//AF070718

F-MAMMA1001751//Human potassium channel KCNQ1 mRNA, complete cds.//1.2e-35:583:65//U90065

F-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.//8.4e-102:627:87//AF041338

F-MAMMA1001757//HS\_2058\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=8 Row=F, genomic survey sequence.//1.7e-24:173:88//AQ243865

F-MAMMA1001760//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-0ligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//6.6e-76:349:87//AL022722

F-MAMMA1001764//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.23:633:57//M97514

F-MAMMA1001768//Bovine herpesvirus 1 complete genome.//2.3e-11:547:60//AJ004801

F-MAMMA1001769//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-76:509:78//AC004801

F-MAMMA1001771//*M. musculus* mRNA for semaphorin B.//2.7e-106:744:82//X859

91

F-MAMMA1001783//Human PAC clone 127H14 from 12q, complete sequence.//6.0e-20:228:75//AC002563

F-MAMMA1001785

F-MAMMA1001788//Human DNA sequence from clone 425C14 on chromosome 6q22  
Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSTF 2) and an unknown gene similar to the placental protein DIFF33 gene. Contains ESTs, STSs and GSSs, complete sequence.//5.0e-05:152:74//Z99129

F-MAMMA1001790//*Homo sapiens* chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//4.5e-53:318:80//AC005845

F-MAMMA1001806//*Homo sapiens* chromosome 19, cosmid R29368, complete sequence.//1.0:131:67//AC004262

F-MAMMA1001812//Human Chromosome X clone bWXD187, complete sequence.//3.0e-34:257:83//AC004383

F-MAMMA1001815//*Homo sapiens* PAC clone DJ0850G01 from 7q21.2-q22, complete sequence.//5.2e-61:516:79//AC004128

F-MAMMA1001817//*Homo sapiens* 12q24 PAC RPCI1-261P5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.1e-32:295:78//AC004031

F-MAMMA1001818//*Homo sapiens* chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//0.71:179:67//AJ011930

F-MAMMA1001820//*Rattus norvegicus* mRNA for PAG608 gene.//3.0e-91:726:79/Y13148

F-MAMMA1001824//HS\_3108\_A1\_G12\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3108 Col=23 Row=M, genomic survey sequence.//3.4e-05:119:74//AQ107508

F-MAMMA1001836//*Homo sapiens* chromosome 18, clone hRPK.537\_E\_1, complete sequence.//3.4e-45:312:85//AC006211

F-MAMMA1001837//*Rattus norvegicus* zinc finger protein Y1 (RLZF-Y) mRNA, complete cds.//4.5e-51:480:75//AF052042

F-MAMMA1001848//CITBI-E1-2516P17.TF CITBI-E1 *Homo sapiens* genomic clone 2516P17, genomic survey sequence.//1.0e-100:486:98//AQ279620

F-MAMMA1001851//Human DNA from overlapping chromosome 19-specific cosmid s R30072 and R28588, genomic sequence, complete sequence.//5.1e-07:197:67//AC002390

F-MAMMA1001854

F-MAMMA1001858//RPCI11-11L22.TP RPCI-11 *Homo sapiens* genomic clone RPCI-11-11L22, genomic survey sequence.//0.091:161:65//B75631

F-MAMMA1001864//Human PAC clone DJ0205E24 from Xq23, complete sequence.//2.6e-09:397:61//AC003013

F-MAMMA1001868//HS\_2196\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2196 Col=24 Row=B, genomic survey sequence.//5.8e-13:86:100//AQ032455

F-MAMMA1001874//*H.sapiens* CpG island DNA genomic Mse1 fragment, clone 63h5, reverse read cpg63h5.rt1a.//1.0:127:63//Z62129

F-MAMMA1001878//Human DNA sequence from BAC 999D10 on chromosome 22q13.3 . Contains two BAC end-sequences (GSSs).//1.7e-19:372:67//Z94802

F-MAMMA1001880//RPCI11-90K3.TJ RPCI11 *Homo sapiens* genomic clone R-90K3, genomic survey sequence.//6.6e-11:362:62//AQ283465

F-MAMMA1001890//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//1.8e-45:317:86//AL021707

F-MAMMA1001907//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//2.7e-23:255:77//Z82207

F-MAMMA1001908//HS\_2225\_A1\_A03\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2225 Col=5 Row=A, genomic survey s

quence.//5.4e-08:264:62//AQ301597

F-MAMMA1001931//HS\_3049\_B2\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=18 Row=H, genomic survey sequence.//1.7e-47:295:90//AQ100157

F-MAMMA1001956//H.sapiens DNA sequence.//0.056:233:66//Z22493

F-MAMMA1001963//Homo sapiens adenylosuccinate lyase gene, complete cds.//0.99:173:68//AF106656

F-MAMMA1001969//Human DNA sequence from cosmid 232L22, between markers D XS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene .//5.3e-63:479:78//Z73986

F-MAMMA1001970//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.4e-126:699:93//AC003071

F-MAMMA1001992//HS\_3078\_A1\_A09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=17 Row=A, genomic survey sequence.//3.3e-08:257:65//AQ143646

F-MAMMA1002009//Homo sapiens chromosome 17, clone hRPK.214\_0\_1, complete sequence.//1.5e-07:244:62//AC005224

F-MAMMA1002011//HS\_3252\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//1.3e-07:170:69//AQ304711

F-MAMMA1002032//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//2.1e-34:315:79//AC004803

F-MAMMA1002033//HS\_3023\_A2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=8 Row=M, genomic survey sequence.//4.3e-69:366:94//AQ105493

F-MAMMA1002041//Genomic sequence from Human 9q34, complete sequence.//5.3e-85:439:82//AC001227

F-MAMMA1002042//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence.//1.4e-20:314:70//AC005669

F-MAMMA1002047//Homo sapiens 12p13.3 BAC RPCI11-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//6.8e-14:526:62//AC05906

F-MAMMA1002056//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiuinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins *S. pombe* C22F3.14C and *C. elegans* C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.1e-47:648:71//AL030996

F-MAMMA1002058//Homo sapiens PAC clone DJ0732C22 from 7p11.2-p13, complete sequence.//2.4e-19:256:74//AC004869

F-MAMMA1002068//Homo sapiens, clone hRPK.2\_A\_1, complete sequence.//5.4e-41:407:78//AC006197

F-MAMMA1002078//Human DNA sequence from PAC 106I20 on chromosome 22q12 Contains ESTs and STS, complete sequence.//0.021:333:64//Z81313

F-MAMMA1002082

F-MAMMA1002084//*Caenorhabditis elegans* cosmid F28C12, complete sequence.//0.032:469:58//Z93380

F-MAMMA1002093//HS\_3050\_B1\_F06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=11 Row=L, genomic survey sequence.//1.0:77:71//AQ105997

F-MAMMA1002108//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5' UTR.//8.3e-10:464:60//AF017308

F-MAMMA1002118

F-MAMMA1002125//Homo sapiens chromosome 17, clone HCIT217L10, complete sequence.//1.0e-35:619:68//AC003962

F-MAMMA1002132//RPCI11-78F11.TJ RPCI11 Homo sapiens genomic clone R-78F1, genomic survey sequence.//1.0e-90:357:97//AQ286460

F-MAMMA1002140//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-45:583:64//AC004216

F-MAMMA1002143//Human serum constituent protein (MSE55) mRNA, complete cds.//6.0e-11:192:70//M88338

F-MAMMA1002145//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE.//0.0028:570:59//AL021391

F-MAMMA1002153//HS\_3005\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=7 Row=G, genomic survey sequence.//4.9e-41:213:99//AQ132213

F-MAMMA1002155//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462023, WORKING DRAFT SEQUENCE.//1.2e-45:303:78//AL031431

F-MAMMA1002156

F-MAMMA1002158//CITBI-E1-2508P18.TR CITBI-E1 Homo sapiens genomic clone 2508P18, genomic survey sequence.//7.1e-42:255:92//AQ266165

F-MAMMA1002170//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//2.0e-81:604:81//AC004448

F-MAMMA1002174//Homo sapiens clone UWGC:y67c126 from 6p21, complete sequence.//3.2e-43:333:83//AC004212

F-MAMMA1002198//H.sapiens thiol-specific antioxidant protein mRNA.//1.0e-34:121:98//Z22548

F-MAMMA1002209//HS\_2197\_B1\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2197 Col=13 Row=J, genomic survey sequence.//9.6e-18:163:84//AQ210058

F-MAMMA1002215//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5' UTR.//6.3e-08:435:60//AF017308

F-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds.//1.8e-124:752:87//AF032667

F-MAMMA1002230//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.67:356:59//AC0

04710

F-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//9.3e-140:836:87//U38253

F-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//1.4e-145:691:98//AC005666

F-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//6.0e-138:660:98//AC005600

F-MAMMA1002267//Homo sapiens chromosome 2, P1 clone 777H5 (LBNL H27), complete sequence.//0.066:333:60//AC003676

F-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//1.1e-39:404:74//AF068748

F-MAMMA1002269//HS\_3163\_B1\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=5 Row=H, genomic survey sequence.//1.0:150:63//AQ171576

F-MAMMA1002282//Human Chromosome 16 BAC clone CIT987SK-327024, complete sequence.//1.5e-22:315:67//AC003108

F-MAMMA1002292//B.garinii (strain TIs1) p83/100 gene (partial).//0.73:20 0:64//X81533

F-MAMMA1002293//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//1.6e-56:408:75//AC006023

F-MAMMA1002294//Sequence 2 from Patent W09516779.//1.8e-06:401:62//A4525 8

F-MAMMA1002297

F-MAMMA1002298//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.0056:525:61//AC004221

F-MAMMA1002299//CIT-HSP-2345B2.TR CIT-HSP Homo sapiens genomic clone 234 5B2, genomic survey sequence.//1.2e-90:446:98//AQ053994

F-MAMMA1002308//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING DRAFT SEQUENCE.//1.3e-35:329:78//AL031680

F-MAMMA1002310//Human gastric (H+ + K+)-ATPase gene, complete cds.//0.00

60:301:60//J05451

F-MAMMA1002311//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.6e-50:327:69//AC004737

F-MAMMA1002312//Homo sapiens DNA sequence from PAC 435D1 on chromosome X q25. Contains ESTs and STS.//1.3e-09:741:58//Z86064

F-MAMMA1002317

F-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//1.9e-158:746:99//AC005756

F-MAMMA1002322//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//5.3e-52:617:70//AC004796

F-MAMMA1002329//Homo sapiens RaP2 interacting protein 8 (RPIP8) mRNA, complete cds.//0.22:143:67//U93871

F-MAMMA1002332//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING DRAFT SEQUENCE.//1.6e-31:287:74//AL034402

F-MAMMA1002333//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162.//2.5e-09:674:59//AL022022

F-MAMMA1002339//Homo sapiens chromosome 21q22.3, cosmid clone Q4H9 complete sequence bases 1..41604.//2.1e-57:522:77//AJ011932

F-MAMMA1002347//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.0e-14:258:69//AC004129

F-MAMMA1002351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1059H15, WORKING DRAFT SEQUENCE.//7.8e-132:723:91//AL022100

F-MAMMA1002352//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 12803, WORKING DRAFT SEQUENCE.//5.8e-17:326:70//Z98742

F-MAMMA1002353//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.1e-14:399:63//AC004825

F-MAMMA1002355//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 109G6, WORKING DRAFT SEQUENCE.//3.7e-43:420:75//AL023879

F-MAMMA1002356//**Plasmodium falciparum** 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:534:59//AC004153

F-MAMMA1002359//**Homo sapiens** 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.3e-18:156:75//AC05831

F-MAMMA1002360//Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST.//4.9e-43:353:69//Z68885

F-MAMMA1002361//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//1.8e-22:282:74//AC008719

F-MAMMA1002362//**Platemys spixii** CR1-like LINE, partial sequence.//0.00058:83:79//D82938

F-MAMMA1002380//CIT-HSP-2383K24.TF CIT-HSP **Homo sapiens** genomic clone 2383K24, genomic survey sequence.//4.4e-10:85:92//AQ196889

F-MAMMA1002384//RPCI11-80J20.TV RPCI11 **Homo sapiens** genomic clone R-80J20, genomic survey sequence.//2.7e-56:286:98//AQ284134

F-MAMMA1002385//CIT-HSP-2328G13.TF CIT-HSP **Homo sapiens** genomic clone 2328G13, genomic survey sequence.//5.5e-46:335:84//AQ043985

F-MAMMA1002392//**Homo sapiens** PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-29:273:78//AC004888

F-MAMMA1002411//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//8.2e-09:287:63//AL023875

F-MAMMA1002413//**Plasmodium falciparum** (strain Dd2) variant-specific surface protein (var-1) gene, complete cds.//9.6e-08:730:57//L40608

F-MAMMA1002417//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING DRAFT SEQUENCE.//4.1e-06:181:72//AL034402

F-MAMMA1002427//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4 , BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//1.3e-51:593:72//AC004604

F-MAMMA1002428

F-MAMMA1002434//Homo sapiens DNA sequence from PAC 958B3 on chromosome X p22.11-Xp22.22. Contains ESTs STS and CpG island.//7.3e-56:388:81//Z93023

F-MAMMA1002446//CIT-HSP-2324022.TR CIT-HSP Homo sapiens genomic clone 23 24022, genomic survey sequence.//2.3e-56:302:95//AQ027479

F-MAMMA1002454//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.1e-54:190:94//AC005229

F-MAMMA1002461//Rattus norvegicus calcium channel alpha-1 subunit gene, partial cds.//0.00045:457:60//U14005

F-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//9.7e-33:709:60//U10556

F-MAMMA1002475//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.092:506:58//AC004671

F-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.025:100:76//AC005077

F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.9e-118:560:98//AF055460

F-MAMMA1002494//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//1.5e-22:297:73//AC005913

F-MAMMA1002498//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//7.2e-10:330:64//AC002477

F-MAMMA1002524//Homo sapiens huntingtin gene, partial exon.//0.0080:124:72//L49359

F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma

ma) mRNA, complete cds.//1.4e-160:775:97//AF065214

F-MAMMA1002545//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//1.9e-41:345:80//AC005696

F-MAMMA1002554

F-MAMMA1002556

F-MAMMA1002566

F-MAMMA1002571//CIT-HSP-2296N17.TR CIT-HSP Homo sapiens genomic clone 22 96N17, genomic survey sequence.//1.7e-07:76:90//AQ006579

F-MAMMA1002573//Homo sapiens DNA, trinucleotide repeats region, clone GAA C27.//2.7e-08:195:70//AB018507

F-MAMMA1002585

F-MAMMA1002590//Homo sapiens BAC clone GS250A16 from 7p21-p22, complete sequence.//2.1e-26:361:69//AC005019

F-MAMMA1002597//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1103G7, WORKING DRAFT SEQUENCE.//1.3e-34:550:69//AL034548

F-MAMMA1002598//H.sapiens mRNA for ribosomal protein L7.//1.1e-21:123:10 0//X57958

F-MAMMA1002603//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//0.0018:358:61//AC005220

F-MAMMA1002612//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//2.1e-13:336:63//AC004861

F-MAMMA1002617//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.14:229:64//AC005486

F-MAMMA1002618

F-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.5e-7 1:319:85//AJ010598

F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds.//1.5e-20:157:9 0//AF041449

F-MAMMA1002623//Homo sapiens T-cell receptor alpha delta locus from base

s 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.

//8.3e-06:137:72//AE000660

F-MAMMA1002625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1056L3, WORKING DRAFT SEQUENCE.//1.9e-171:819:98//AL031727

F-MAMMA1002629//Human BAC clone RG385F02 from 7p15, complete sequence.//4.8e-85:478:78//AC003093

F-MAMMA1002636//Human POU domain factor (Brn-3a) gene, exon 2, complete cds.//5.6e-09:499:62//U10063

F-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//3.6e-115:785:82//AF055666

F-MAMMA1002646//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.5e-45:291:90//AC002038

F-MAMMA1002650//Homo sapiens candidate tumor suppressor HIC-1 (HIC-1) gene, complete cds.//6.6e-06:661:59//L41919

F-MAMMA1002655//HS\_2003\_A2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2003 Col=22 Row=A, genomic survey sequence.//9.0e-15:198:74//AQ224233

F-MAMMA1002662

F-MAMMA1002665//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.4e-37:235:84//AC005029

F-MAMMA1002671//Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.//0.00027:272:64//U22398

F-MAMMA1002673

F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//3.7e-161:752:99//D86987

F-MAMMA1002685//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 394I7, WORKING DRAFT SEQUENCE.//6.2e-45:510:70//AL023585

F-MAMMA1002698//HS\_3024\_B1\_C06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3024 Col=11 Row=F, genomic survey

sequence.//1.7e-10:155:75//AQ072214

F-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//5.9e-75:509:83//AF018261

F-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//1.2e-159:749:99//AB011399

F-MAMMA1002708//Human DNA sequence from clone 267M20 on chromosome Xq22.

2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//3.0e-57:347:79//AL031053

F-MAMMA1002711//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//3.4e-31:484:69//AC005030

F-MAMMA1002721//CIT-HSP-2350M5.TR CIT-HSP Homo sapiens genomic clone 2350M5, genomic survey sequence.//1.4e-06:265:63//AQ061245

F-MAMMA1002727//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence.//0.18:386:58//AL023584

F-MAMMA1002728//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase. (EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//3.2e-05:362:63//Z83821

F-MAMMA1002744//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//0.00010:535:58//AE001368

F-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//1.2e-182:880:97//AC005856

F-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.7e-175:829:98//AC006055

F-MAMMA1002754//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT S  
EQUENCE, 1 ordered pieces.//3.1e-31:372:75//AC004676

F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds.//3.3e-26:151:98  
//AB007902

F-MAMMA1002764//Human Chromosome 11 Cosmid cSRL166a1, complete sequence.  
//5.2e-49:355:81//U73636

F-MAMMA1002765//RPCI11-20A22.TPB RPCI-11 Homo sapiens genomic clone RPCI  
-11-20A22, genomic survey sequence.//6.7e-13:155:76//B92153

F-MAMMA1002769//CIT-HSP-2323G1.TF CIT-HSP Homo sapiens genomic clone 232  
3G1, genomic survey sequence.//9.7e-21:151:90//AQ028244

F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M860  
4 Met protein (M8604 Met) gene, complete cds.//5.6e-105:179:99//U07561

F-MAMMA1002780//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from contig 3-08, complete sequence.//0.071:277:58//Z98546

F-MAMMA1002782//HS\_3213\_B2\_B08\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3213 Col=16 Row=D, genomic survey  
sequence.//0.00018:219:63//AQ175845

F-MAMMA1002796

F-MAMMA1002807//Human Chromosome X PAC RPCI1-290C9 from the Pieter de Jo  
ng Human PAC library; complete sequence.//6.9e-22:332:69//AC002404

F-MAMMA1002820//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Pa  
rk Cancer Institute Human PAC Library) complete sequence.//5.9e-11:483:6  
2//AC003035

F-MAMMA1002830//Homo sapiens chromosome 17, clone hCIT529I10, complete s  
equence.//1.0e-64:320:83//AC002553

F-MAMMA1002833//Homo sapiens PAC clone DJ0745K06 from 7q31, complete seq  
uence.//2.8e-47:413:80//AC004875

F-MAMMA1002835

F-MAMMA1002838//A-916H10.TP CIT978SK Homo sapiens genomic clone A-916H10

, genomic survey sequence.//1.1e-39:164:83//B14462

F-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete  
cds.//1.9e-62:373:81//U58883

F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds.//1.  
7e-135:635:99//AB018353

F-MAMMA1002844//F1707-T7 IGF Arabidopsis thaliana genomic clone F1707, g  
enomic survey sequence.//6.7e-17:383:66//B11616

F-MAMMA1002858

F-MAMMA1002868//RPCI11-54F9.TJ RPCI11 Homo sapiens genomic clone R-54F9,  
genomic survey sequence.//8.3e-81:392:99//AQ081566

F-MAMMA1002869//Sequence 1 from patent US 5552529.//2.2e-86:696:78//I258  
63

F-MAMMA1002871//Lupinus angustifolius nodulin-45 gene, complete cds.//0.  
029:370:59//L12388

F-MAMMA1002880//RPCI11-23M23.TV RPCI-11 Homo sapiens genomic clone RPCI-  
11-23M23, genomic survey sequence.//1.8e-20:271:74//B86518

F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete  
cds.//1.2e-28:680:61//D45027

F-MAMMA1002886//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 380A1, WORKING DRAFT SEQUENCE.//0.00040:505:57//Z97653

F-MAMMA1002887//HS\_3238\_B2\_G08\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3238 Col=16 Row=N, genomic survey  
sequence.//5.5e-79:401:97//AQ219814

F-MAMMA1002890//Mus musculus MHC class III region RD gene, partial cds;  
Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t, and smRNP genes, complete c  
ds; G7A gene, partial cds; and unknown genes.//4.6e-35:136:73//AF109906

F-MAMMA1002892//Mouse Cosmid ma66a100 from 14D1-D2, complete sequence.//  
5.7e-14:450:60//AC004096

F-MAMMA1002895//H.sapiens CpG island DNA genomic Msel fragment, clone 46

b6, forward read cpg46b6.ft1a.//3.7e-36:190:100//Z58616  
F-MAMMA1002908//Penaeus monodon microsatellite locus Pmo27.//1.1e-05:195  
:62//AF068828  
F-MAMMA1002909//Human Chromosome 11 pac pDJ205d23, complete sequence.//1  
.0e-13:457:61//AC002402  
F-MAMMA1002930//Homo sapiens Xp22 BAC GSHB-512P14 (Genome Systems Human  
BAC library) complete sequence.//0.25:260:62//AC004467  
F-MAMMA1002937//H.sapiens ZNF74-1 mRNA.//6.3e-13:577:59//X71623  
F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds.//5  
.1e-193:910:98//AB014598  
F-MAMMA1002941//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCR  
L2-GGT Region, complete sequence.//2.7e-23:174:77//AC004032  
F-MAMMA1002947//Rhodobacter capsulatus strain SB1003, partial genome.//1  
.3e-09:475:61//AF010496  
F-MAMMA1002964//Human thiopurine methyltransferase (TPMT) gene, exon 5./  
/0.0029:314:60//AF019366  
F-MAMMA1002970//Human DNA sequence from PAC 436M11 on chromosome Xp22.11  
-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and  
the first coding exon of the RS1 gene for retinoschisis (X-linked, juve  
nile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//4.0  
e-10:194:71//Z94056  
F-MAMMA1002972//H.sapiens CpG island DNA genomic Mse1 fragment, clone 2g  
10, forward read cpg2g10.ft1aa.//0.38:156:66//Z55272  
F-MAMMA1002973//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, comple  
te sequence.//2.9e-41:234:79//AC005919  
F-MAMMA1002982//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6  
p24.1-p25.3.//1.7e-05:322:63//AL022098  
F-MAMMA1002987//CITBI-E1-2514J12.TR CITBI-E1 Homo sapiens genomic clone  
2514J12, genomic survey sequence.//0.0064:135:66//AQ275871

F-MAMMA1003003//cSRL-145D12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-145D12, genomic survey sequence.//2.8e-31:201:89//B01998

F-MAMMA1003004//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y237C10, WORKING DRAFT SEQUENCE.//1.6e-10:180:73//AL031601

F-MAMMA1003007//Homo sapiens (clone cosmid c11q-8D1) tetranucleotide repeat polymorphism at the D11S488 locus.//3.5e-12:435:61//L04732

F-MAMMA1003011//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//2.3e-50:734:67//U79139

F-MAMMA1003013//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.2e-86:341:79//AC003694

F-MAMMA1003015//Homo sapiens Chromosome 16 BAC clone CIT987SK-591M7, complete sequence.//2.6e-13:443:61//AC003661

F-MAMMA1003019//HS\_3221\_A1\_A01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=1 Row=A, genomic survey sequence.//2.8e-51:299:92//AQ184271

F-MAMMA1003026

F-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//0.0037:134:73//AC005214

F-MAMMA1003035//RPCI11-11P4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11P4, genomic survey sequence.//1.1e-07:66:100//B74936

F-MAMMA1003039//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.1e-19:220:76//AC004671

F-MAMMA1003040//Human DNA sequence from PAC 340N1 on chromosome 1p35-36.  
2. Contains ESTs, polymorphic CA repeat, tRNA and endogenous retrovirus.  
//9.5e-91:469:78//Z98257

F-MAMMA1003044//Human DNA sequence from clone 496N17 on chromosome 6p11.  
2-12.3 Contains EST, GSS, complete sequence.//0.21:289:61//AL031321

F-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein  
PIASy mRNA, complete cds.//1.7e-139:663:98//AF077952

F-MAMMA1003049

F-MAMMA1003055//HS\_3014\_B2\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=20 Row=L, genomic survey sequence.//4.2e-05:215:64//AQ164940

F-MAMMA1003056//HS\_3221\_B2\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=24 Row=H, genomic survey sequence.//1.4e-16:206:74//AQ302772

F-MAMMA1003057//M. domesticus MD6 mRNA.//8.5e-128:654:94//X54352

F-MAMMA1003066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 273F20, WORKING DRAFT SEQUENCE.//1.0:142:71//AL034371

F-MAMMA1003089//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.7e-42:373:78//AC004796

F-MAMMA1003099//Homo sapiens beta-filamin mRNA, complete cds.//2.6e-42:288:88//AF042166

F-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//1.6e-12:477:64//U72634

F-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//3.4e-121:789:85//AF071316

F-MAMMA1003127//R. norvegicus MYR1 mRNA for myosin I heavy chain.//9.4e-58:423:83//X68199

F-MAMMA1003135//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.62:676:58//U67916

F-MAMMA1003140

F-MAMMA1003146//Homo sapiens mRNA for Galt3 protein.//2.2e-80:397:97//Y15062

F-MAMMA1003150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 598F2, WORKING DRAFT SEQUENCE.//7.3e-123:266:88//AL021579

F-MAMMA1003166//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 250D10, WORKING DRAFT SEQUENCE.//1.6e-33:143:82//Z99716

F-NT2RM1000001//Human DNA sequence from clone 393P23 on chromosome Xq21.  
1-21.33. Contains GSSs, complete sequence.//0.50:216:61//Z95400

F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//4.8e-65:385:  
92//D31886

F-NT2RM1000032

F-NT2RM1000035//Cricetulus griseus SREBP cleavage activating protein (SC  
AP) mRNA, complete cds.//6.3e-135:565:84//U67060

F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.  
1e-106:542:95//AB014590

F-NT2RM1000039//Mouse genetic suppressor element mRNA.//0:080:239:60//L2  
7155

F-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//8.4e-9  
6:535:91//D87671

F-NT2RM1000059//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600

F-NT2RM1000062//Nephila clavipes dragline silk protein spidroin 1 gene,  
partial cds.//0.54:306:63//U37520

F-NT2RM1000080//Sequence 2 from patent US 5763589.//1.5e-115:566:97//AR0  
12692

F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//1  
.8e-114:550:97//AB014561

F-NT2RM1000092//Homo sapiens chromosome 19, cosmid R26894, complete sequ  
ence.//0.63:180:65//AC005594

F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.0  
27:126:70//AF007155

F-NT2RM1000119//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 466N1, WORKING DRAFT SEQUENCE.//0.022:644:58//Z97630

F-NT2RM1000127//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5,  
genomic survey sequence.//1.6e-45:254:94//AQ195884

F-NT2RM1000131//Homo sapiens mRNA for KIAA0792 protein, complete cds.//5  
.5e-153:778:95//AB018335

F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit  
mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1  
e-90:448:97//AF044959

F-NT2RM1000153//Human NotI linking clone 924A081D, genomic survey sequence.//5.9e-07:66:96//U49890

● F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.0  
25:126:70//AF007155

F-NT2RM1000187//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2  
510J4, genomic survey sequence.//1.1e-05:56:98//AQ261184

F-NT2RM1000199//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//1.6e-38:711:65//D64009

F-NT2RM1000242

F-NT2RM1000244//HS\_2229\_A1\_C04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2229 Col=7 Row=E, genomic survey sequence.//2.0e-13:95:95//AQ298474

● F-NT2RM1000252//Homo sapiens chromosome 17, clone hRPK.206\_C\_20, complete sequence.//0.023:225:61//AC006070

F-NT2RM1000256//Caenorhabditis elegans cosmid F22B3, complete sequence.//  
8.5e-24:473:64//Z68336

F-NT2RM1000257//Homo sapiens MAGOH mRNA, complete cds.//6.4e-69:455:85//  
AF035940

F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds.//6.5e-57:460  
:80//D50920

F-NT2RM1000271

F-NT2RM1000272

F-NT2RM1000280//Bos gaurus vacuolar H-ATPase subunit D (VATD) mRNA, complete cds.//6.7e-97:430:92//U11927

F-NT2RM1000300//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//2.1e-96:170:100//Z93097

F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds.//8.1e-127:70 8:92//D63880

F-NT2RM1000318//Homo sapiens mRNA for ribosomal protein L39, complete cds.//5.7e-34:182:99//D79205

F-NT2RM1000341//Homo sapiens full length insert cDNA clone YP11F06.//1.3e-100:504:97//AF085879

F-NT2RM1000354//HS\_2001\_B1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//1.6e-11:201:73//AQ218494

F-NT2RM1000355//Mus musculus E25B protein mRNA, complete cds.//1.8e-77:5 78:82//U76253

F-NT2RM1000365//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces.//9.4e-113:367:97//AC004821

F-NT2RM1000377//H.sapiens mRNA for MAP kinase phosphatase 4.//6.1e-14:36 2:62//Y08302

F-NT2RM1000388//Azospirillum brasilense lateral flagellin (laf1) gene, complete cds.//1.0:482:58//U26679

F-NT2RM1000394//M.musculus mRNA for histone H3.3A.//1.7e-94:549:89//Z859 79

F-NT2RM1000399

F-NT2RM1000421//HS\_2213\_B1\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//3.6e-08:195:72//AQ032737

F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//3.7e-84:418:97//AF084928

F-NT2RM1000499//Human mRNA for KIAA0167 gene, complete cds.//1.3e-35:525  
:69//D79989

F-NT2RM1000539//Homo sapiens PAC clone DJ1194E14 from 7p21, complete seq  
uence.//4.6e-73:533:83//AC004993

F-NT2RM1000553

F-NT2RM1000555//Homo sapiens clone 24514 unknown mRNA.//2.3e-110:555:97/  
/AF070542

F-NT2RM1000563//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6  
unordered pieces.//1.3e-123:477:100//AC004873

F-NT2RM1000623//HS\_2213\_B1\_E01\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey s  
equence.//8.2e-06:75:89//AQ032737

F-NT2RM1000648//Halobium cutirubrum L11, L1, L10 and L12 equivalent ribo  
somal protein gene cluster.//1.3e-06:414:61//X15078

F-NT2RM1000661//Homo sapiens cap-binding protein 4EHP mRNA, complete cds  
.//9.3e-54:275:97//AF047695

F-NT2RM1000666//HS\_2016\_B2\_H08\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2016 Col=16 Row=P, genomic survey  
sequence.//5.7e-13:199:73//AQ227865

F-NT2RM1000669//Human DNA sequence from clone 281H8 on chromosome 6q25.1  
-25.3. Contains up to four novel genes, one with similarity to KIAA0323  
and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the  
latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a puta  
tive CpG island and genomic marker D6S1553, complete sequence.//2.7e-94:  
499:94//AL031133

F-NT2RM1000672

F-NT2RM1000691//Homo sapiens HRIHFB2060 mRNA, partial cds.//2.2e-119:582  
:98//AB015348

F-NT2RM1000699//Caenorhabditis elegans cosmid Y41C4A, complete sequence.

//0.95:284:61//AL032627

F-NT2RM1000702//HS\_3005\_A1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.073:290:58//AQ089514

F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase.//4.8e-65:435:85//AJ004832

F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds.//8.0e-126:690:92//AB011139

F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//2.5e-66:524:83//AF027208

F-NT2RM1000746//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//0.92:395:58//AJ011930

F-NT2RM1000770//Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds.//2.1e-70:407:92//L39210

F-NT2RM1000772//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.6e-36:98:93//AC000380

F-NT2RM1000780//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//9.3e-22:126:99//X52233

F-NT2RM1000781//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.1e-09:540:59//AC004153

F-NT2RM1000800//Mus musculus mRNA for B-IND1 protein.//4.0e-81:497:88//Z97207

F-NT2RM1000802

F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//3.7e-63:490:84//AF027208

F-NT2RM1000826//Homo sapiens clone 24514 unknown mRNA.//7.2e-153:749:96//AF070542

F-NT2RM1000829//HS\_3047\_A1\_A05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.74:215:67//AQ099134

F-NT2RM1000833//Canis familiaris sec61 homologue mRNA, complete cds.//5.1e-114:683:88//M96629

F-NT2RM1000850//F.rubripes GSS sequence, clone 163A22aF11, genomic survey sequence.//1.1e-26:279:74//AL018762

F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//9.3e-148:726:97//AJ010840

● F-NT2RM1000857//Rattus norvegicus gene for cytochrome P450/6 beta B, exon 2.//0.97:124:65//AB008378

F-NT2RM1000867//H.sapiens DNA sequence surrounding NotI site, clone NRLA 143D.//1.2e-31:172:98//X95834

F-NT2RM1000874//Homo sapiens KE05 protein mRNA, complete cds.//2.8e-131:632:97//AF064605

F-NT2RM1000882//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.//1.2e-98:214:99//AC004228

● F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//2.7e-156:762:97//AF082516

F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds.//2.0e-17:310:67//AB014561

F-NT2RM1000894//Mus musculus second largest subunit of RNA polymerase I (RPA2) mRNA, complete cds.//3.2e-95:469:83//U58280

F-NT2RM1000898

F-NT2RM1000905//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//1.8e-74:188:98//Z97630

F-NT2RM1000924//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-148:601:98//AC004873

F-NT2RM1000927//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21  
unordered pieces.//0.071:392:60//AC004846

F-NT2RM1000962//H.sapiens CpG island DNA genomic Mse1 fragment, clone 14  
0d1, forward read cpg140d1.ft1a.//4.1e-35:187:99//Z56803

F-NT2RM1000978//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRA  
FT SEQUENCE, 2 ordered pieces.//1.1e-23:266:77//AC005959

F-NT2RM1001003//Homo sapiens alpha-catenin-like protein mRNA, complete c  
ds.//4.0e-160:760:98//U97067

F-NT2RM1001008//Kaposi's sarcoma-associated herpes-like virus ORF73 homo  
log gene, complete cds.//1.7e-11:602:61//U52064

F-NT2RM1001043//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-X  
p11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repe  
ats.//3.9e-93:645:86//Z95125

F-NT2RM1001044//S.pombe chromosome III cosmid c320.//0.90:128:66//AL0222  
45

F-NT2RM1001059//Homo sapiens chromosome 5, Bac clone 58g14 (LBNL H76), c  
omplete sequence.//3.8e-53:261:80//AC005915

F-NT2RM1001066//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 21  
72N17, genomic survey sequence.//0.64:285:59//B94391

F-NT2RM1001072//HS\_3115\_B1\_D07\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3115 Col=13 Row=H, genomic survey  
sequence.//7.3e-23:140:95//AQ147905

F-NT2RM1001074//Homo sapiens chromosome 19, cosmid F20489, complete sequ  
ence.//5.0e-50:186:98//AC005263

F-NT2RM1001082//Sequence 1 from Patent W09718303.//2.1e-144:736:95//A627

31

F-NT2RM1001085//CIT-HSP-2310F21.TR CIT-HSP Homo sapiens genomic clone 23  
10F21, genomic survey sequence.//8.8e-45:235:97//AQ020757

F-NT2RM1001092//HS\_3055\_B1\_G05\_MF CIT Approved Human Genomic Sperm Libra

ry D *Homo sapiens* genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.1e-89:471:95//AQ155489

F-NT2RM1001102//Human HEM45 mRNA, complete cds.//1.2e-28:482:63//U88964

F-NT2RM1001105//*Homo sapiens* hRED1 gene, exon 1 (5' UTR).//0.0014:349:61//Z95973

F-NT2RM1001112//*Homo sapiens* chromosome 19, cosmid R34094, complete sequence.//0.060:429:58//AC004678

F-NT2RM1001115//*Plasmodium falciparum* merozoite surface protein 3 (MSP-3) gene, partial cds.//0.93:156:62//AF024624

F-NT2RM1001139//*Homo sapiens* chromosome 19, fosmid 37502, complete sequence.//1.2e-10:466:59//AC004755

F-NT2RM2000006//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//5.3e-150:724:98//AL031291

F-NT2RM2000013//*D.melanogaster* DmRP128 gene for RNA polymerase III second-largest subunit.//1.5e-58:749:69//X58826

F-NT2RM2000030//*Homo sapiens* clone DJ0708P22, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.1e-97:270:77//AC004863

F-NT2RM2000032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-25:172:76//AL034379

F-NT2RM2000042//Human DNA sequence from cosmid U55E4, between markers DX S6791 and DXS8038 on chromosome X contains ESTs.//5.0e-05:325:65//Z73418

F-NT2RM2000092//*Homo sapiens* (D8S321 locus) DNA sequence, tetranucleotide repeat polymorphism.//0.63:117:68//L12269

F-NT2RM2000093//*Mus musculus* major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG 24, NG25, and NG26 genes, complete cds; and unknown genes.//0.38:312:62//AF109905

F-NT2RM2000101

F-NT2RM2000124//Mouse cAMP-dependent protein kinase catalytic subunit mR

NA, complete cds.//3.8e-58:297:97//M12303

F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A2 (PDE9A) mRNA, complete cds.//3.8e-138:653:98//AF067224

F-NT2RM2000192//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 217 2B3, genomic survey sequence.//2.2e-33:191:95//B93289

F-NT2RM2000239//F.rubripes GSS sequence, clone 156P04aG12, genomic survey sequence.//8.9e-44:445:69//AL018549

F-nnnnnnnnnnnnn//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds.//0.00020:380:61//AF075292

● F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds.//3.1e-128:615:98//AB011162

F-NT2RM2000259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310013, WORKING DRAFT SEQUENCE.//0.0013:305:63//AL031658

F-NT2RM2000260//Mus musculus WW domain binding protein 15 mRNA, partial sequence.//3.0e-14:645:61//AF073934

● F-NT2RM2000287//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//1.3e-11:96:86//AC003656

● F-NT2RM2000322//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//8.5e-115:233:97//AL031864

F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//8.8e-175:805:99//AB011132

F-NT2RM2000363//RPCI11-90B10.TJ RPCI11 Homo sapiens genomic clone R-90B10, genomic survey sequence.//6.7e-15:96:98//AQ285300

F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA

, partial cds.//1.2e-94:599:86//U48251

F-NT2RM2000371//RPCI11-57I4.TJ RPCI11 Homo sapiens genomic clone R-57I4, genomic survey sequence.//1.1e-52:312:91//AQ083343

F-NT2RM2000374//M. musculus nodal gene, a TGF-beta-like gene.//6.7e-31:1 96:91//X70514

F-NT2RM2000395//Leishmania major chromosome 1, complete sequence.//0.99: 345:58//AE001274

F-NT2RM2000402//Arabidopsis thaliana BAC T19D16 genomic sequence.//2.1e- 23:414:63//U95973

● F-NT2RM2000407//Mus musculus semaphorin VIa mRNA, complete cds.//1.4e-13 1:439:88//AF030430

F-NT2RM2000420//HS\_3063\_B2\_F11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//3.2e-25:154:95//AQ103204

F-NT2RM2000422//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.// 1.7e-128:782:86//L22022

F-NT2RM2000452//HS\_3009\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=10 Row=H, genomic survey sequence.//1.2e-16:122:90//AQ130794

● F-NT2RM2000469//HS\_2019\_A1\_G02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2019 Col=3 Row=M, genomic survey sequence.//9.6e-22:176:85//AQ229041

F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds.//7. 5e-15:386:63//AB018290

F-NT2RM2000502

F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds. //5.1e-171:824:97//AF061243

F-NT2RM2000522

F-NT2RM2000540

F-NT2RM2000556//*Homo sapiens* 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.9e-42:344:82//AC04466

F-NT2RM2000566//*Homo sapiens* integrin alpha-7 mRNA, complete cds.//2.8e-154:751:97//AF072132

F-NT2RM2000567//*Pseudomonas aeruginosa* enoyl-CoA hydratase gene, partial cds; pilin biosynthetic protein (fimL) gene, complete cds; and unknown gene.//3.0e-06:664:58//AF083252

F-NT2RM2000569//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//1.3e-15:348:67//AL031681

F-NT2RM2000577//RPCI11-43G22.TJ RPCI11 *Homo sapiens* genomic clone R-43G22, genomic survey sequence.//1.6e-14:155:80//AQ199391

F-NT2RM2000581//*Homo sapiens* mRNA for KIAA0214 protein, complete cds.//5.4e-174:820:98//D86987

F-NT2RM2000588//*Homo sapiens* 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.1e-60:344:82//AC04466

F-NT2RM2000594//*Mus musculus* DNA cytosine-5 methyltransferase 3B1 (Dnmt3b) mRNA, alternatively spliced, complete cds.//4.9e-118:761:85//AF068626

F-NT2RM2000599//*O. sativa* osr40g3 gene.//0.30:585:56//Y08988

F-NT2RM2000609

F-NT2RM2000612//*Rattus norvegicus* ADP-ribosylation factor-directed GTPases activating protein mRNA, complete cds.//7.8e-102:709:83//U35776

F-NT2RM2000623//*Homo sapiens* chromosome 19, cosmid F19847, complete sequence.//3.4e-17:450:65//AC005952

F-NT2RM2000624

2.9e-06:231:64//Z82061

F-NT2RM2000635//*Homo sapiens* mRNA for KIAA0729 protein, partial cds.//6.3e-142:664:98//AB018272

F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//7.

4e-138:664:98//AB014558

F-NT2RM2000639//RPCI11-69E5.TJ RPCI11 Homo sapiens genomic clone R-69E5,  
genomic survey sequence.//3.7e-14:97:97//AQ267491

F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.

1e-167:518:99//AB014576

F-NT2RM2000669

F-NT2RM2000691//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete  
sequence.//1.1e-106:748:82//AC002038

● F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds.//6.8e-49:748:  
64//D86984

F-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//2.4e-124:594  
:98//AB015342

F-NT2RM2000735//Human ZNF43 mRNA.//8.4e-111:756:82//X59244

F-NT2RM2000740//Mus musculus lymphocyte specific helicase mRNA, complete  
cds.//1.3e-141:815:89//U25691

F-NT2RM2000795//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 439F8, WORKING DRAFT SEQUENCE.//1.0e-78:723:76//AL021392

● F-NT2RM2000821//Rat mRNA for beta COP.//2.0e-150:879:88//X57228

● F-NT2RM2000837//Homo sapiens BAC clone GS214N13 from 7p14-p15, complete  
sequence.//1.1e-05:361:62//AC005017

F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//  
8.7e-184:847:99//AB015046

F-NT2RM2000952

F-NT2RM2000984//Mus musculus major histocompatibility locus class III re  
gions Hsc70t gene, partial cds; s<sub>m</sub>RNP, G7A, NG23, MutS homolog, CLCP, NG  
24, NG25, and NG26 genes, complete cds; and unknown genes.//7.6e-41:239:  
76//AF109905

F-NT2RM2001004//CIT-HSP-2333N18.TR CIT-HSP Homo sapiens genomic clone 23

33N18, genomic survey sequence.//1.1e-11:298:66//AQ035862

F-NT2RM2001035//Mus musculus mCAF1 protein mRNA, complete cds.//1.4e-120  
:627:91//U21855

F-NT2RM2001065//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete  
cds.//6.8e-118:690:88//AF071314

F-NT2RM2001100//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6  
unordered pieces.//2.3e-145:614:99//AC004873

F-NT2RM2001105//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 50024, WORKING DRAFT SEQUENCE.//2.7e-95:461:99//AL034380

● F-NT2RM2001131//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog  
gene, complete cds.//7.2e-24:726:62//U52064

F-NT2RM2001141

F-NT2RM2001152//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq  
21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//0.98:300:62//AL022401

F-NT2RM2001177//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15  
unordered pieces.//1.2e-147:741:96//AC005488

● F-NT2RM2001194//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes,  
complete cds, UL8 gene, partial cds.//0.026:408:59//U66829

F-NT2RM2001196//Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//2.2e-135:627:98//AC004987

F-NT2RM2001201//Mus musculus clone OST431, genomic survey sequence.//6.1  
e-80:503:86//AF046700

F-NT2RM2001221//Chimpanzee (P.paniscus) involucrin, complete cds.//0.53:  
670:55//M26514

F-NT2RM2001238//Rat glutaminase mRNA, complete cds.//3.4e-128:719:90//M6  
5150

F-NT2RM2001243

F-NT2RM2001247//CITBI-E1-2521M18.TR CITBI-E1 Homo sapiens genomic clone 2521M18, genomic survey sequence.//0.0011:274:59//AQ276184

F-NT2RM2001256//M.musculus mRNA for 200 kD protein.//2.3e-129:742:90//X8 0169

F-NT2RM2001291//CIT-HSP-2010I15.TR CIT-HSP Homo sapiens genomic clone 20 10I15, genomic survey sequence.//4.6e-09:156:72//B57734

F-NT2RM2001306//RPCI11-28I5.TP RPCI-11 Homo sapiens genomic clone RPCI-1 1-28I5, genomic survey sequence.//0.069:234:64//B84850

F-NT2RM2001312//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//1.1e-22:111:81//AC005919

F-NT2RM2001319//Borrelia burgdorferi (section 4 of 70) of the complete genome.//0.99:340:58//AE001118

F-NT2RM2001324//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 209H1, WORKING DRAFT SEQUENCE.//3.7e-44:340:85//Z84465

F-NT2RM2001345//HS\_3005\_A1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.042:290:58//AQ089514

F-NT2RM2001360//Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.//5.0e-60:365:87//U56429

F-NT2RM2001370//Homo sapiens PAC clone DJ0815D20 from 7p11-p13, complete sequence.//0.98:415:58//AC004899

F-NT2RM2001393//Homo sapiens Chromosome 22q11.2 PAC Clone p\_m11 In BCRL2 -GGT Region, complete sequence.//4.0e-54:394:75//AC004033

F-NT2RM2001420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//2.8e-169:789:99//AL033520

F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.1e-96:453:99//AJ007509

F-NT2RM2001499//Rattus norvegicus mRNA for cationic amino acid transport

er 3, complete cds.//7.1e-91:601:83//AB000113

F-NT2RM2001504//Homo sapiens chromosome 19, cosmid R30017, complete sequence.//0.81:200:69//AC005624

F-NT2RM2001524//Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No. 2.//3.8e-16:316:65//Z99708

F-NT2RM2001544

F-NT2RM2001547//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//3.3e-24:318:67//AL032657

F-NT2RM2001575//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//2.1e-26:582:64//M34551

F-NT2RM2001582//M.musculus red-1 gene.//1.4e-102:581:90//X92750

F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds.//7.0e-10:282:65//AB007902

F-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//9.6e-131:736:90//AF032667

F-NT2RM2001605//RBP2=retinoblastoma binding protein 2 [human, Nalm-6 pre-B cell leukemia, mRNA, 6455 nt].//2.3e-85:749:75//S66431

F-NT2RM2001613//Rattus rattus sec61 homologue mRNA, complete cds.//8.6e-118:779:85//M96630

F-NT2RM2001632//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//1.5e-50:561:71//AC004691

F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//9.2e-153:740:98//AB014518

F-NT2RM2001637//F.rubripes GSS sequence, clone 155D22bD8, genomic survey sequence.//2.5e-13:224:64//Z91020

F-NT2RM2001641//CIT-HSP-2347F23.TF CIT-HSP Homo sapiens genomic clone 2347F23, genomic survey sequence.//1.3e-67:340:98//AQ060913

F-NT2RM2001648//Canis familiaris sec61 homologue mRNA, complete cds.//1.4e-110:459:89//M96629

F-NT2RM2001652//*Bos taurus* guanine nucleotide-exchange protein (ARF-GEP1)  
mRNA, complete cds.//1.2e-153:807:93//AF023451

F-NT2RM2001659//nbxb0002cE07f CUGI Rice BAC Library *Oryza sativa* genomic  
clone nbxb0002J13f, genomic survey sequence.//1.0:485:56//AQ051653

F-NT2RM2001664//*Homo sapiens* IkappaB kinase complex associated protein (IKAP)  
mRNA, complete cds.//3.7e-172:802:99//AF044195

F-NT2RM2001668

F-NT2RM2001670//*Homo sapiens* complete genomic sequence between D16S3070  
and D16S3275, containing Familial Mediterranean Fever gene disease.//3.2  
e-18:279:70//AJ003147

F-NT2RM2001671//*Oryctolagus cuniculus* sarcolemmal associated protein-3 m  
RNA, complete cds.//1.6e-137:683:94//U21157

F-NT2RM2001675//RPCI11-51J16.TJ RPCI11 *Homo sapiens* genomic clone R-51J1  
6, genomic survey sequence.//1.0:394:58//AQ053677

F-NT2RM2001681//*Arabidopsis thaliana* DNA chromosome 4, BAC clone T805 (E  
SSAII project).//0.87:220:61//AL021890

F-NT2RM2001688//*B. parapertussis* bvg locus (transcription regulators of v  
irulence factors) with bvgA and bvgS genes.//1.0:286:62//X52948

F-NT2RM2001695//CIT-HSP-345H13.TVB CIT-HSP *Homo sapiens* genomic clone 34  
5H13, genomic survey sequence.//3.2e-53:241:82//B59854

F-NT2RM2001696//Mouse DNA with homology to EBV IR3 repeat, segment 2, cl  
one Mu2.//1.2e-05:306:58//M10668

F-NT2RM2001698//*Homo sapiens* DNA sequence from PAC 163M9 on chromosome 1  
p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseud  
ogene, ESTs, STS, GSS, complete sequence.//6.0e-06:548:59//AL021920

F-NT2RM2001699//HS\_3195\_B2\_D01\_T7 CIT Approved Human Genomic Sperm Libra  
ry D *Homo sapiens* genomic clone Plate=3195 Col=2 Row=H, genomic survey s  
equence.//2.7e-07:322:61//AQ189056

F-NT2RM2001700//*Mycobacterium tuberculosis* H37Rv complete genome; segmen

t 109/162.//7.8e-05:354:58//Z95556

F-NT2RM2001706//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//7.5e-42:335:81//AC004469

F-NT2RM2001716

F-NT2RM2001718//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//4.2e-08:536:58//AC004290

F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence.//1.4e-26:163:95//AF052123

F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//6.2e-111:530:98//AB007931

F-NT2RM2001730//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//3.1e-02:248:95//AJ010598

F-NT2RM2001743

F-NT2RM2001753//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.11:138:66//Z68117

F-NT2RM2001760//Canis familiaris sec61 homologue mRNA, complete cds.//9.4e-100:418:88//M96629

F-NT2RM2001768//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993

F-NT2RM2001771//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.3e-66:680:72//AC006116

F-NT2RM2001782

F-NT2RM2001784//Bovine herpesvirus type 1 (Cooper) DNA (30 kb).//0.027:384:60//Z48053

F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770

F-NT2RM2001797//HS\_3045\_A1\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3045 Col=1 Row=G, genomic survey s

equence.//1.4e-74:381:97//AQ129456

F-NT2RM2001800

F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.3e-178:827:99//AF044195

F-NT2RM2001805//Malus domestica leucine-rich receptor-like protein kinase (LRPKm1) gene, 5' flanking region and 5' UTR.//1.0:290:58//AF053126

F-NT2RM2001813//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 21 69F21, genomic survey sequence.//3.3e-16:109:95//B89870

F-NT2RM2001823//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence.//5.8e-62:819:68//AC004274

F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//3.6e-1 31:738:90//AF013759

F-NT2RM2001840//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.1e-57:422:79//AC002347

F-NT2RM2001855//HS\_3224\_A1\_H07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3224 Col=13 Row=0, genomic survey sequence.//0.00012:68:91//AQ205285

F-NT2RM2001867//Human DNA sequence from clone 889N15 on chromosome Xq22. 1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.068:1 02:70//AL031177

F-NT2RM2001879//Human DNA sequence from cosmid cU72E5, between markers D XS366 and DXS87 on chromosome X.//0.0029:500:59//Z68328

F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//1.9e-187:866:97//AB014610

F-NT2RM2001896//S.cerevisiae chromosome III complete DNA sequence.//8.6e

-30:613:63//X59720

F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.

9e-176:859:97//AB007931

F-NT2RM2001930//M. musculus mRNA for semaphorin G.//4.7e-117:730:85//X978

18

F-NT2RM2001935//Sequence 11 from Patent WO9610637.//1.0:356:60//A50028

F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence./  
/6.9e-138:653:98//AF091080

F-NT2RM2001950//RPCI11-24L12.TP RPCI-11 Homo sapiens genomic clone RPCI-  
11-24L12, genomic survey sequence.//2.7e-19:188:81//B86700

F-NT2RM2001982//Arabidopsis thaliana chromosome II BAC T24I21 genomic se  
quence, complete sequence.//0.42:179:65//AC005825

F-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, com  
plete cds.//3.8e-20:123:98//AF089816

F-NT2RM2001989//Sequence 3 from patent US 5747317.//1.9e-167:786:98//AR0  
04981

F-NT2RM2001997//Human HepG2 partial cDNA, clone hmd1b08m5.//9.6e-25:160:  
95//D16955

F-NT2RM2001998//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 co  
mplete sequence, encoding carbonyl reductase and carbonyl reductase 3 (c  
omplete cds).//0.88:380:60//AB003151

F-NT2RM2002004//Human Chromosome X, complete sequence.//5.0e-88:831:77//  
AC002407

F-NT2RM2002014

F-NT2RM2002030//Mus musculus glutamine:fructose-6-phosphate amidotransfe  
rase mRNA, complete cds.//1.5e-89:822:74//U00932

F-NT2RM2002049//Bovine elastin mRNA, partial cds.//8.8e-11:125:81//M2613

2

F-NT2RM2002055

F-NT2RM2002088//*Mus musculus* WW domain binding protein 17 mRNA, partial sequence.//1.4e-15:421:63//AF073936

F-NT2RM2002091//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.//4.6e-160:771:98//AL034380

F-NT2RM2002100//*Homo sapiens* mRNA for ATP-dependent RNA helicase, partial.//7.7e-164:776:98//AJ010840

F-NT2RM2002109//*Homo sapiens* glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//2.4e-143:684:98//AF030435

F-NT2RM2002128//*Mesocricetus auratus* guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, complete cds.//7.0e-27:330:73//U13152

F-NT2RM2002142//*Danio rerio* gastrulation specific (G12) mRNA, complete cds.//6.3e-10:135:80//U27121

F-NT2RM2002145//*Homo sapiens* erythroblast macrophage protein EMP mRNA, complete cds.//4.2e-143:800:92//AF084928

F-NT2RM2002178//*Homo sapiens* mRNA for KIAA0467 protein, partial cds.//5.2e-164:787:97//AB007936

F-NT2RM2002580//*Drosophila melanogaster* DNA sequence (P1 DS02110 (D147)), complete sequence.//7.4e-13:337:62//AC004423

F-NT2RM4000024//*D. melanogaster* DmRP128 gene for RNA polymerase III second-largest subunit.//1.2e-62:801:70//X58826

F-NT2RM4000027//*Caenorhabditis elegans* cosmid F09E5.//0.36:336:60//U37429

F-NT2RM4000030//*H. sapiens* CpG island DNA genomic Mse1 fragment, clone 56h10, forward read cpg56h10.ft1a.//9.3e-22:127:100//Z55685

F-NT2RM4000046//*Cucurbita maxima* 25S - 18S rDNA intergenic spacer.//4.1e-05:386:60//X13059

F-NT2RM4000061

F-NT2RM4000085//*B. taurus* mRNA for nuclear DNA helicase II.//1.9e-10:485:59//X82829

F-NT2RM4000086

F-NT2RM4000104//*Homo sapiens* chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds.//4.2e-23:345:69//AF060865

F-NT2RM4000139//*R. norvegicus* trg mRNA.//1.4e-56:708:69//X68101

F-NT2RM4000155//CIT-HSP-2282N15.TR CIT-HSP *Homo sapiens* genomic clone 2282N15, genomic survey sequence.//3.0e-09:88:90//AQ0000070

F-NT2RM4000156//*H. sapiens* HPBRII-7 gene.//2.0e-21:586:60//X67336

F-NT2RM4000167//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.7e-143:810:90//D12646

F-NT2RM4000169//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0054:746:57//AC004157

F-NT2RM4000191//*Mus musculus* cathepsin S (CatS) gene, promoter region and exons 1 and 2.//0.00018:468:60//AF051726

F-NT2RM4000197

F-NT2RM4000199//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//0.67:461:60//AL031667

F-NT2RM4000200

F-NT2RM4000202//*H. sapiens* CpG island DNA genomic Mse1 fragment, clone 34c2, forward read cpg34c2.ft1a.//1.7e-27:190:90//Z65361

F-NT2RM4000210//*Homo sapiens* mRNA for KIAA0712 protein, complete cds.//1.4e-182:856:98//AB018255

F-NT2RM4000215//*S. cerevisiae* MAK16 protein gene, complete cds, and LTE1 protein gene, 3' end.//3.1e-31:731:62//J03852

F-NT2RM4000229//*Homo sapiens* chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//4.6e-102:233:94//AC005383

F-NT2RM4000233//*Mus musculus* semaphorin VIa mRNA, complete cds.//1.6e-135:835:86//AF030430

F-NT2RM4000244//RPCI11-24P15.TV RPCI-11 *Homo sapiens* genomic clone RPCI-

11-24P15, genomic survey sequence.//5.5e-08:422:62//B86757  
F-NT2RM4000251//Mus musculus clone UWGC:mbac92 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//0.98:207:60//AC005855  
F-NT2RM4000265//Homo sapiens Chromosome 11q12.2 PAC clone pDJ1081b4 containing human mRNA for T-cell glycoprotein CD6, complete sequence.//5.2e-41:707:65//AC003689  
F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//7.9e-153:609:93//M99438  
F-NT2RM4000324  
● F-NT2RM4000327//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds.//3.9e-44:727:68//AF022085  
F-NT2RM4000344//Mus musculus ATP-dependent metalloprotease FtsH1 mRNA, complete cds.//1.0e-143:801:90//AF090430  
F-NT2RM4000349//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700  
F-NT2RM4000354//HS\_2221\_A2\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221 Col=14 Row=E, genomic survey sequence.//1.0e-20:180:83//AQ253449  
F-NT2RM4000356  
● F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//1.6e-133:628:99//AB014542  
F-NT2RM4000368//RPCI11-91B5.TJ RPCI11 Homo sapiens genomic clone R-91B5, genomic survey sequence.//5.0e-12:431:61//AQ283217  
F-NT2RM4000386//Mus musculus DOC4 (Doc4) mRNA, complete cds.//7.4e-86:845:72//AF059485  
F-NT2RM4000395//Saccharomyces cerevisiae chromosome VI cosmid 9965.//2.5e-34:767:61//D44597  
F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.5e-15:114:94//AB015046

F-NT2RM4000421

F-NT2RM4000425//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//1.5e-37:295:82//AC005921

F-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//3.9e-94:740:78//AF062476

F-NT2RM4000457//CIT-HSP-2346B17.TR CIT-HSP Homo sapiens genomic clone 23 46B17, genomic survey sequence.//1.5e-22:149:92//AQ062111

F-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//1.3e-76:386:97//AJ010952

● F-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22A, //1.1e-22:356:67//AB000459

F-NT2RM4000496//Homo sapiens 12p13.3 BAC RPCI11-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.53:198:70//AC005908

F-NT2RM4000511

F-NT2RM4000514

F-NT2RM4000515//CIT-HSP-2285L3.TR CIT-HSP Homo sapiens genomic clone 228 5L3, genomic survey sequence.//0.0012:200:66//AQ000113

● F-NT2RM4000520

● F-NT2RM4000531//Human zinc finger protein 42 (MZF-1) mRNA, complete cds. //2.9e-31:732:64//M58297

F-NT2RM4000532//HS\_3231\_B1\_C05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3231 Col=9 Row=F, genomic survey sequence.//1.3e-59:362:90//AQ192093

F-NT2RM4000534

F-NT2RM4000585//CITBI-E1-2508I18.TR CITBI-E1 Homo sapiens genomic clone 2508I18, genomic survey sequence.//1.1e-34:208:93//AQ260706

F-NT2RM4000590//CIT-HSP-2291M14.TF CIT-HSP Homo sapiens genomic clone 2291M14, genomic survey sequence.//8.3e-34:180:99//AQ004125

F-NT2RM4000595//*Homo sapiens* chromosome 17, clone hCIT.131\_K\_11, complete sequence.//1.2e-09:203:66//AC005288

F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds.//5.3e-14:305:68//AB002390

F-NT2RM4000611//CIT-HSP-2169F21.TR CIT-HSP *Homo sapiens* genomic clone 21 69F21, genomic survey sequence.//8.4e-16:109:94//B89870

F-NT2RM4000616//*D.melanogaster* mRNA for acetyl-CoA synthetase.//2.3e-59:721:68//Z46786

F-NT2RM4000674

F-NT2RM4000689//CIT-HSP-2381013.TF CIT-HSP *Homo sapiens* genomic clone 23 81013, genomic survey sequence.//2.6e-31:174:97//AQ110303

F-NT2RM4000698

F-NT2RM4000700

F-NT2RM4000712//*Homo sapiens* ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//1.1e-89:744:77//AF022789

F-NT2RM4000717

F-NT2RM4000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//2.1e-140:299:99//AL034379

F-NT2RM4000734//*Homo sapiens* mRNA for KIAA0760 protein, partial cds.//3.8e-158:743:98//AB018303

F-NT2RM4000741

F-NT2RM4000751//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//7.1e-95:754:77//M99593

F-NT2RM4000764

F-NT2RM4000778//*Caenorhabditis elegans* cosmid F36H12.//0.30:523:60//AF078790

F-NT2RM4000779//*Homo sapiens* mRNA for KIAA0451 protein, complete cds.//5.5e-172:810:98//AB007920

F-NT2RM4000787//Human DNA sequence from PAC 370M22 on chromosome 22q12-q

ter. contains GRB2 ADAPTOR LIKE PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (UQCRCFS1) exon, ESTs, STS, CA repeat and CpG island.//0.0057:163:69//Z82206

F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//6.9e-39:237:94//AC005306

F-NT2RM4000795//Rattus norvegicus neuroligin 3 mRNA, complete cds.//5.9e-97:857:74//U41663

F-NT2RM4000796//HS\_3214\_B1\_F11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=21 Row=L, genomic survey sequence.//1.1e-14:254:68//AQ175988

F-NT2RM4000798//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//6.2e-78:816:72//AF023451

F-NT2RM4000813//Leishmania major glycoprotein 96-92 (GP 96-92) gene, partial cds.//0.33:276:63//M63109

F-NT2RM4000820//, complete sequence.//2.6e-142:450:97//AC005406

F-NT2RM4000833//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//1.9e-52:501:71//AC004373

F-NT2RM4000848//Homo sapiens chromosome 17, clone hRPK.167\_N\_20, complete sequence.//1.0:477:56//AC005940

F-NT2RM4000852

F-NT2RM4000855//Homo sapiens chromosome 17, clone hCIT.457\_L\_16, complete sequence.//3.4e-29:229:83//AC003957

F-NT2RM4000887

F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds.//2.1e-20:407:64//AB011004

F-NT2RM4000950//Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces.//0.41:311:64//AC004929

F-NT2RM4000971//RPCI11-53H3.TJ RPCI11 Homo sapiens genomic clone R-53H3, genomic survey sequence.//1.0:208:64//AQ053735

F-NT2RM4000979//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence.//1.3e-19:207:78//AC005245

F-NT2RM4000996//CITBI-E1-2506B10.TF CITBI-E1 Homo sapiens genomic clone 2506B10, genomic survey sequence.//1.4e-73:361:98//AQ263651

F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//5.1e-170:803:98//AB018272

F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//3.3e-125:584:99//AB014539

F-NT2RM4001032//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.00034:777:58//U47276

F-NT2RM4001047//M025 gene [mice, embryos, mRNA, 2322 nt].//2.5e-92:776:74//S51858

F-NT2RM4001054//Canis familiaris sec61 homologue mRNA, complete cds.//3.1e-102:859:76//M96629

F-NT2RM4001084//CIT-HSP-2330F9.TR CIT-HSP Homo sapiens genomic clone 2330F9, genomic survey sequence.//4.6e-78:379:99//AQ044479

F-NT2RM4001092//cSRL-71b1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-71b1, genomic survey sequence.//1.1e-12:152:75//B05776

F-NT2RM4001116

F-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.9e-136:717:93//AC004593

F-NT2RM4001151//Streptomyces antibioticus ATP-binding protein and membrane protein (oleC-ORF1, oleC-ORF2, oleC-ORF3, oleC-ORF4, and oleC-ORF5) genes, complete cds; 3427 base-pairs.//0.0083:368:60//L06249

F-NT2RM4001155//Bos taurus 50 kDa protein (adp50) mRNA, complete cds.//3.9e-120:764:85//U04706

F-NT2RM4001160

F-NT2RM4001187

F-NT2RM4001191//CIT-HSP-2010E7.TF CIT-HSP Homo sapiens genomic clone 201

0E7, genomic survey sequence.//6.2e-12:181:72//B53378

F-NT2RM4001200//H.sapiens HZF10 mRNA for zinc finger protein.//1.3e-66:7  
99:69//X78933

F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete c  
ds.//4.2e-152:707:99//AF004828

F-NT2RM4001204

F-NT2RM4001217//Homo sapiens ectoderm-neural cortex-1 protein (ENC-1) mR  
NA, complete cds.//1.6e-62:715:70//AF005381

F-NT2RM4001256//Human NotI linking clone 924A058R, genomic survey sequen  
ce.//7.6e-14:109:90//U49884

F-NT2RM4001258//HS\_3171\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3171 Col=18 Row=N, genomic survey  
sequence.//2.5e-18:215:77//AQ149676

F-NT2RM4001309//Human DNA sequence from clone 551E13 on chromosome Xp11.  
2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protei  
n pseudogene, EST, GSS, complete sequence.//4.9e-28:526:66//AL022163

F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase.//2.5e-  
77:474:89//Z46973

F-NT2RM4001316//Caenorhabditis elegans cosmid K09H11.//1.2e-16:230:73//U  
97002

F-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.//1.1e  
-41:642:66//D89016

F-NT2RM4001340//EP(3)0614 Drosophila melanogaster EP line Drosophila mel  
anogaster genomic Sequence recovered from 5' end of P element, genomic s  
urvey sequence.//0.0040:141:68//AQ025127

F-NT2RM4001344//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y1E3, WORKING DRAFT SEQUENCE.//5.5e-06:469:60//AL021388

F-NT2RM4001347

F-NT2RM4001371//Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence.//0.10:400:61//AC004786

F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//2.2e-167:790:98//AF098799

F-NT2RM4001384//Homo sapiens DNA sequence from BAC 747E2 on chromosome 2q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//0.99:255:59//AL021393

F-NT2RM4001410//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//0.027:336:58//AP000023

F-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds.//5.9e-124:783:85//AF020526

F-NT2RM4001412//Rattus norvegicus GTPase activating protein SynGAP-c mRNA, complete cds.//2.2e-34:418:71//AF050183

F-NT2RM4001414//Homo sapiens full length insert cDNA clone ZE16C11.//9.1e-76:363:100//AF086563

F-NT2RM4001437//Homo sapiens chromosome 5, BAC clone 313n8 (LBNL H146), complete sequence.//2.0e-47:623:69//AC004226

F-NT2RM4001444//Streptococcus pneumoniae penicillin-binding protein 2b (pbp2b), RecM (recM), D-Ala-D-Ala ligase (ddl), D-Ala-D-Ala adding enzyme (murF), MutT (mutT), cell division protein FtsA (ftsA), cell division protein FtsZ (ftsZ), YlmE (ylmE), YlmF (ylmF), YlmG (ylmG), YlmH (ylmH), cell division protein DivIVA (divIVA), and isoleucine-tRNA synthetase (ileS) genes, complete cds; and unknown gene.//3.6e-09:566:58//AF068901

F-NT2RM4001454

F-NT2RM4001455

F-NT2RM4001483//Human zinc finger protein ZNF136.//3.2e-36:329:78//U0936

7

F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//1.2e-155:724:99//AB014585

F-NT2RM4001519//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00019:418:59//AC004688

F-NT2RM4001522//Human HepG2 3' region MboI cDNA, clone hmd6a08m3.//1.4e-16:130:88//D17274

F-NT2RM4001557

F-NT2RM4001565

F-NT2RM4001566

F-NT2RM4001569//HS\_2050\_B1\_C08\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2050 Col=15 Row=F, genomic survey sequence.//2.7e-09:109:84//AQ234720

F-NT2RM4001582//*Mus musculus* COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//1.2e-127:740:89//AF071317

F-NT2RM4001592//*M. musculus* mRNA of enhancer-trap-locus 1.//7.3e-117:710:88//X69942

F-NT2RM4001594//*Homo sapiens* chromosome 9q34, clone 107G20, WORKING DRAFT SEQUENCE, 2 ordered pieces.//0.34:388:59//AC002355

F-NT2RM4001597//*M. musculus* red-1 gene.//6.2e-139:788:90//X92750

F-NT2RM4001605//*Homo sapiens* mRNA for KIAA0791 protein, complete cds.//3.3e-162:750:99//AB018334

F-NT2RM4001611//*Synechocystis* sp. PCC6803 complete genome, 12/27, 143041 9-1576592.//2.5e-05:490:58//D90910

F-NT2RM4001629//*Mus musculus* palmytoylated protein p55 mRNA, complete cds.//0.65:186:64//U38196

F-NT2RM4001650//\*\*\* SEQUENCING IN PROGRESS \*\*\* *Homo sapiens* chromosome 4, BAC clone C0435P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.99:422:59//AC004689

F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds.//2.6e-81:449:93//AB002320

F-NT2RM4001666

F-NT2RM4001682//*Mus musculus* clone OST9187, genomic survey sequence.//3.

2e-35:240:87//AF046699

F-NT2RM4001710//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//1.9e-151:564:97//AL031447

F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds.//7.0e-85:748:74//D86957

F-NT2RM4001715//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.2e-91:488:94//AL034430

● F-NT2RM4001731//Orang-utan involucrin gene, complete cds.//0.40:530:59//M25312

F-NT2RM4001741//Mouse mRNA for talin.//1.1e-129:737:90//X56123

F-NT2RM4001746//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316G12, WORKING DRAFT SEQUENCE.//2.3e-49:320:89//AL031709

F-NT2RM4001754//*Homo sapiens* 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//6.3e-64:379:76//AC005831

F-NT2RM4001758//*R.norvegicus* mRNA for serine/threonine kinase MARK1.//3.

7e-146:871:87//Z83868

● F-NT2RM4001776//*Homo sapiens* mRNA for KIAA0727 protein, partial cds.//2.3e-173:803:99//AB018270

F-NT2RM4001783//*Homo sapiens* clone DJ0981007, complete sequence.//2.0e-165:593:99//AC006017

F-NT2RM4001810

F-NT2RM4001813//*Homo sapiens* BAC clone NH0364H22 from 2, complete sequence.//7.1e-31:176:84//AC005036

F-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//4.4e-34:195:95//M37712

F-NT2RM4001823//*Mus musculus* zinc finger protein (Zfp64) mRNA, complete

cds.//3.3e-51:490:75//U49046

F-NT2RM4001828//Human zinc finger containing protein ZNF157 (ZNF157) mRNA, complete cds.//5.6e-74:688:72//U28687

F-NT2RM4001836//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete sequence.//1.0:406:60//AC000076

F-NT2RM4001841//Mus musculus A kinase anchor protein (AKAP-KL) mRNA, alternatively spliced isoform 2, complete cds.//1.6e-131:831:86//AF033275

F-NT2RM4001842//HS\_3163\_A2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=20 Row=M, genomic survey sequence.//1.5e-05:355:60//AQ168513

F-NT2RM4001856//Caenorhabditis elegans cosmid K08F11.//4.0e-23:823:60//U70855

F-NT2RM4001858//Notophthalmus viridescens NvTbox1 mRNA, partial cds.//6.4e-11:266:66//U64433

F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//6.9e-149:704:98//Y17711

F-NT2RM4001876//F.rubripes GSS sequence, clone 060E22bA4, genomic survey sequence.//5.7e-48:600:68//Z88651

F-NT2RM4001880//CIT-HSP-2348J1.TF CIT-HSP Homo sapiens genomic clone 2348J1, genomic survey sequence.//0.0025:61:88//AQ060809

F-NT2RM4001905//R.norvegicus CYP3A1 gene, 5' flanking region.//2.5e-29:535:67//X98335

F-NT2RM4001922//HS\_2237\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//2.2e-73:364:98//AQ033732

F-NT2RM4001930//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MXI10, complete sequence.//4.9e-10:269:63//AB005248

F-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//7.6e-152:311:100//AC005207

F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//1.1e-170:808:98//AF098162

F-NT2RM4001953//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B13E4; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.7e-45:310:86//AC004046

F-NT2RM4001965//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//1.6e-107:622:90//AB020868

F-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//3.9e-24:221:76//X99  
330

F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.0e-61:527:76//AB018341

F-NT2RM4001984//Human DNA sequence from cosmid U151E3, between markers on chromosome X.//5.8e-07:502:60//Z82253

F-NT2RM4001987//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//2.6e-33:177:99//AQ051701

F-NT2RM4002013//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//0.019:65:90//AC005921

F-NT2RM4002018//Human high molecular weight B cell growth factor mRNA sequence.//1.0:527:57//L15344

F-NT2RM4002034//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//0.11:322:60//AL008712

F-NT2RM4002044//Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds.//0.015:513:61//U01882

F-NT2RM4002054//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.0e-44:473:76//AC005283

F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds.//1.0e-171:803:98//AB014540

F-NT2RM4002062//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3  
; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0031:  
298:59//AC005122

F-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, comp  
lete cds.//1.1e-147:705:98//U82267

F-NT2RM4002066//Human mRNA for KIAA0192 gene, partial cds.//3.4e-73:889:  
69//D83783

F-NT2RM4002067//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192),  
complete sequence.//1.1e-53:295:76//AC005216

● F-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partia  
l cds.//7.8e-25:277:75//AF072758

F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete  
cds.//9.0e-23:588:61//AF059569

F-NT2RM4002093//Rat PYBP1 mRNA for pyrimidine binding protein 1.//3.1e-6  
8:544:69//X60789

F-NT2RM4002109//Mouse kif4 mRNA for microtubule-based motor protein KIF4  
, complete cds.//2.0e-121:762:86//D12646

● F-NT2RM4002128//HS\_3084\_A1\_D04\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey s  
equence.//7.7e-18:117:95//AQ186312

F-NT2RM4002140

F-NT2RM4002145//Homo sapiens chromosome 19, fosmid 37308, complete seque  
nce.//1.8e-49:736:65//AC004152

F-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.5e-70:454:85//  
AF035940

F-NT2RM4002161//Homo sapiens mRNA for LAFPTPase, isoform 1, partial.//4.  
2e-151:763:96//AJ130763

F-NT2RM4002174//Helicobacter pylori 26695 section 18 of 134 of the compl  
ete genome.//2.1e-16:580:60//AE000540

F-NT2RM4002189//Homo sapiens DNA sequence from BAC 722E9 on chromosome 2

2q13.2-13.33. Contains ESTs.//1.0e-07:792:61//AL008636

F-NT2RM4002194//Mus musculus semaphorin VIA mRNA, complete cds.//3.2e-13

2:782:87//AF030430

F-NT2RM4002205//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//1.5e-40:292:84//L14684

F-NT2RM4002213

F-NT2RM4002226//Mus musculus p190-B gene, complete cds.//0.099:350:59//U67160

● F-NT2RM4002251//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//1.0:428:58//AC004448

F-NT2RM4002256//Mouse genomic DNA, chromosome 17, clone cosmid 49.1, genomic survey sequence.//9.4e-60:294:81//AB005959

F-NT2RM4002266//Fugu rubripes GSS sequence, clone 006I18aG12, genomic survey sequence.//3.3e-12:217:67//AL024779

F-NT2RM4002278//HS\_3089\_A1\_E05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3089 Col=9 Row=I, genomic survey sequence.//1.9e-64:381:92//AQ121653

F-NT2RM4002281

● F-NT2RM4002287//CIT-HSP-2327E14.TF CIT-HSP Homo sapiens genomic clone 2327E14, genomic survey sequence.//9.0e-49:336:86//AQ042515

F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds.//2.1e-48:511:72//D87457

F-NT2RM4002301//Human NotI linking clone 924A053D, genomic survey sequence.//8.9e-05:62:91//U49881

F-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudogene similar to GPISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//4.9e-115:729:87//AL032822

F-NT2RM4002339//*Homo sapiens* PAC clone DJ0728D04, complete sequence.//1.

1e-97:457:93//AC004865

F-NT2RM4002344//*Caenorhabditis elegans* cosmid K04A8.//2.2e-06:190:69//U6  
4849

F-NT2RM4002373//*Homo sapiens* mRNA for KIAA0649 protein, complete cds.//2  
.8e-149:708:98//AB014549

F-NT2RM4002374//*Homo sapiens* 12q24 PAC P336P3 (Research Park Cancer Institute Human Genome PAC library) complete sequence.//0.00040:312:63//AC00  
2978

F-NT2RM4002383//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//6.8e-29:378:66//AL031284

F-NT2RM4002390

F-NT2RM4002398//CIT-HSP-2288N22.TR CIT-HSP *Homo sapiens* genomic clone 22  
88N22, genomic survey sequence.//3.4e-35:184:100//AQ001110

F-NT2RM4002409//*Archaeoglobus fulgidus* section 15 of 172 of the complete genome.//2.0e-16:468:59//AE001092

F-NT2RM4002438//Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence.//1.6e-16:123:91//U89336

F-NT2RM4002446//Human DNA sequence from cosmid 443D9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs, STS and CpG islands.//9.6e-64:467:84//Z92845

F-NT2RM4002452

F-NT2RM4002457//Human DNA sequence from PAC 151B14 on chromosome 22, complete sequence.//2.2e-24:201:86//Z85988

F-NT2RM4002460//*Homo sapiens* PAC clone DJ0630C24 from 7q31-q32, complete sequence.//1.3e-45:487:70//AC004690

F-NT2RM4002479//*Homo sapiens* RNA helicase-related protein mRNA, complete

cds.//2.7e-163:777:98//AF083255

F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//2  
.3e-93:464:97//AB014591

F-NT2RM4002493

F-NT2RM4002499//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3  
unordered pieces.//3.5e-41:442:75//AC005484

F-NT2RM4002504//Human DNA sequence from clone 391022 on chromosome 6p21.  
2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, c  
omplete sequence.//3.8e-31:233:87//AL031577

F-NT2RM4002527//Fugu rubripes GSS sequence, clone 096G17aC8, genomic sur  
vey sequence.//7.7e-08:274:62//AL027162

F-NT2RM4002532

F-NT2RM4002534

F-NT2RM4002558//Mus musculus fatty acid transport protein 4 mRNA, partia  
l cds.//3.8e-53:394:81//AF072759

F-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//6.4e-160:902:89//  
AF022962

F-NT2RM4002567//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2  
503J7, genomic survey sequence.//8.5e-31:220:88//AQ263402

F-NT2RM4002571//Rattus norvegicus UDP-GalNAc:polypeptide N-acetylgalacto  
saminytransferase T5 mRNA, complete cds.//5.2e-05:199:65//AF049344

F-NT2RM4002593//Homo sapiens PAC clone DJ0745K06 from 7q31, complete seq  
uence.//0.89:275:61//AC004875

F-NT2RM4002594//Drosophila melanogaster, chromosome 2R, region 31C1-31D6  
, P1 clone DS08879, complete sequence.//3.7e-44:768:64//AC005454

F-NT2RM4002623//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3  
; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-34  
:574:65//AC005122

F-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//3.9e-111:582:95

//AB013385

F-NT2RP1000035//*Homo sapiens* mRNA for NS1-binding protein (NS1-BP).//1.1  
e-153:747:96//AJ012449

F-NT2RP1000040//*Homo sapiens* genomic DNA, chromosome 21q11.1, segment 18  
/28, WORKING DRAFT SEQUENCE.//1.6e-125:243:88//AP000047

F-NT2RP1000063//*Caenorhabditis elegans* cosmid F31C3, complete sequence./  
/9.6e-09:414:59//Z92784

F-NT2RP1000086//*H.sapiens* mRNA for zinc finger protein, Hsal2.//2.8e-183  
:548:91//X98834

F-NT2RP1000101//*H.sapiens* CpG island DNA genomic Mse1 fragment, clone 28  
b4, forward read cpg28b4.ft1a.//6.0e-27:163:95//Z60555

F-NT2RP1000111//CIT-HSP-2307014.TR CIT-HSP *Homo sapiens* genomic clone 23  
07014, genomic survey sequence.//1.2e-11:128:81//AQ016069

F-NT2RP1000112//Human kinase (TTK) mRNA, complete cds.//1.0e-38:324:81//  
M86699

F-NT2RP1000124//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from MAL4P1, WORKING DRAFT SEQUENCE.//0.59:476:59//AL034557

F-NT2RP1000130//DNA encoding human Hepatoma-derived Growth Factor.//2.7e  
-35:535:68//E08546

F-NT2RP1000163//*Homo sapiens* cell cycle progression 2 protein (CPR2) mRNA  
A, complete cds.//6.7e-05:77:90//AF011792

F-NT2RP1000170//*Homo sapiens* clone NH0001P09, WORKING DRAFT SEQUENCE, 1  
unordered pieces.//1.9e-20:431:64//AC006030

F-NT2RP1000174//*Homo sapiens* clone 24432 mRNA sequence.//2.5e-138:679:97  
//AF070535

F-NT2RP1000191

F-NT2RP1000202//Porcine mRNA for M130 of smooth muscle myosin phosphatase,  
partial cds.//5.3e-05:220:61//D89496

F-NT2RP1000243//*Drosophila melanogaster* DNA sequence (P1 DS05273 (D80)),

complete sequence.//4.7e-51:508:69//AC004373

F-NT2RP1000259

F-NT2RP1000272//Mus musculus TLS-associated protein with SR repeats mRNA  
, complete cds.//7.8e-142:866:88//AF042383

F-NT2RP1000324//RPCI11-81021.TJ RPCI11 Homo sapiens genomic clone R-8102  
1, genomic survey sequence.//2.8e-29:182:92//AQ285136

F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding  
mitochondrial protein, complete cds.//4.2e-147:693:98//AF053551

F-NT2RP1000333//Caenorhabditis elegans cosmid C03D6, complete sequence./  
/1.4e-08:281:61//Z75525

F-NT2RP1000348//H.sapiens CpG island DNA genomic Msel fragment, clone 12  
f1, reverse read cpgl2f1.rt1c.//1.7e-09:71:100//Z56610

F-NT2RP1000357

F-NT2RP1000358

5.7e-16:403:61//AC005456

F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds.//9.  
8e-125:497:86//AB014538

F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA,  
complete cds.//1.8e-176:877:96//AF064594

F-NT2RP1000409//Homo sapiens repetitive sequences, alphoid DNA, 2482bp./  
/4.6e-106:700:84//AJ001558

F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//9  
.4e-178:710:98//AB011159

F-NT2RP1000416

F-NT2RP1000418//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3  
' end of cds.//1.0:198:60//L40178

F-NT2RP1000439//HS\_2182\_A1\_D06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=G, genomic survey  
sequence.//2.1e-68:441:87//AQ024305

F-NT2RP1000443//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18  
/28, WORKING DRAFT SEQUENCE.//3.8e-57:185:88//AP000047

F-NT2RP1000460//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete  
sequence.//2.7e-132:204:99//AC004453

F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, gen  
omic sequence, complete sequence.//4.9e-80:196:95//AC002985

F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, comp  
lete cds.//1.9e-55:440:80//U47634

F-NT2RP1000481//Homo sapiens DNA sequence from PAC 262D12 on chromosome  
1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin,  
Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S rib  
osomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, g  
enomic marker D1S2691 and STSs.//2.6e-92:562:88//Z99297

F-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//2  
.0e-130:622:98//D87686

F-NT2RP1000513//Xanthomonas campestris campestris xpsD, xpsM, and xpsN g  
enes, complete cds's.//0.11:360:58//M81648

F-NT2RP1000522//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8  
unordered pieces.//4.9e-34:209:93//AC004895

F-NT2RP1000547//Cricetulus griseus COP-coated vesicle membrane protein C  
HOp24 mRNA, partial cds.//1.2e-08:331:63//U26264

F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partia  
l cds.//4.4e-81:295:92//AF017418

F-NT2RP1000577//HS\_2228\_B2\_C05\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2228 Col=10 Row=F, genomic survey  
sequence.//1.9e-31:179:75//AQ185128

F-NT2RP1000581//Pan troglodytes von Willebrand factor (vWF) gene, partia  
l cds.//4.7e-34:223:90//U31620

F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730)

containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770

F-NT2RP1000629//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.3e-89:584:84//M62419

F-NT2RP1000630//Human DNA sequence from PAC 151B14 on chromosome 22 Contains EST, complete sequence.//1.0:203:63//Z85989

F-NT2RP1000677//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//0.0034:350:61//AC005943

F-NT2RP1000688//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//5.2e-10:120:80//X69907

F-NT2RP1000695

F-NT2RP1000701//Sequence 1 from patent US 5580968.//2.4e-99:624:86//I305  
36

F-NT2RP1000721//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3  
unordered pieces.//1.1e-19:188:81//AC004932

F-NT2RP1000730

F-NT2RP1000733//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//1.3e-30:315:75//U95742

F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//8.0e-122:604:96//AF101434

F-NT2RP1000746//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=0, genomic survey sequence.//1.5e-83:466:92//AQ186344

F-NT2RP1000767//Homo sapiens full length insert cDNA clone ZD81B04.//2.8e-21:144:91//AF086442

F-NT2RP1000782//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840

F-NT2RP1000796//T. thermophilus phosphofructokinase 1 (PFK1) gene, complete cds.//0.76:263:64//M71213

F-NT2RP1000825//Human DNA sequence from clone 116F5 on chromosome 22q13.

Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSSs, GSSs, genomic marker D2 2S1168 and a CA repeat polymorphism, complete sequence.//1.5e-77:163:96//Z93244

F-NT2RP1000833//Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA, complete cds.//1.3e-147:424:96//AF048837

F-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-89:702:79//AF047020

F-NT2RP1000836//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF 6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//8.7e-169:842:96//AL022398

F-NT2RP1000846//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//3.3e-15:196:76//U96629

F-NT2RP1000851//Homo sapiens PAC clone 267D11 from 12, complete sequence.//1.6e-144:724:96//AC004812

F-NT2RP1000856//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840

F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//6.7e-106:551:95//AF064094

F-NT2RP1000902//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING DRAFT SEQUENCE.//0.0097:55:100//Z82199

F-NT2RP1000915//H.sapiens genomic DNA fragment (clone J32A032R).//1.3e-3 0:174:97//Z94761

F-NT2RP1000916

F-NT2RP1000943//Hylobates lar huntingtin gene, partial exon.//0.19:103:7 2//L49362

F-NT2RP1000944//HS\_2179\_B2\_C12\_MR CIT Approved Human Genomic Sperm Libra

ry D *Homo sapiens* genomic clone Plate=2179 Col=24 Row=F, genomic survey sequence.//0.032:140:63//AQ065269

F-NT2RP1000947//*Mus musculus* ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//3.7e-53:461:78//U62483

F-NT2RP1000954//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid *Homo sapiens* genomic clone cSRL-143G4, genomic survey sequence.//0.030:89:78//B01950

F-NT2RP1000958//*Caenorhabditis elegans* cosmid K01C8, complete sequence.//3.9e-11:445:61//Z49068

● F-NT2RP1000959//*Homo sapiens* PAC clone 278C19 from 12q, complete sequence.//3.3e-57:326:92//AC004263

F-NT2RP1000966//Human nucleolin gene, complete cds.//3.4e-64:197:98//M60858

F-NT2RP1000980//CIT-HSP-2314B10.TF CIT-HSP *Homo sapiens* genomic clone 2314B10, genomic survey sequence.//0.32:137:68//AQ017126

F-NT2RP1000988//Human chromosome 3p21.1 gene sequence.//8.0e-72:665:80//L13435

● F-NT2RP1001011//*Drosophila melanogaster* DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//1.3e-31:497:65//U34925

● F-NT2RP1001013//HS\_3068\_B1\_B09\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3068 Col=17 Row=D, genomic survey sequence.//1.0e-24:414:66//AQ127667

F-NT2RP1001014//HS\_3252\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//0.00052:83:81//AQ304711

F-NT2RP1001033//*Homo sapiens* chromosome 17, clone hRPC.1073\_F\_15, complete sequence.//1.3e-134:241:99//AC004686

F-NT2RP1001073//*Homo sapiens* PAC clone DJ1194E14 from 7p21, complete sequence.//2.5e-59:451:83//AC004993

F-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//4.5e-93:476:96//U82267

F-NT2RP1001080//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//6.6e-54:217:89//AC004938

F-NT2RP1001113

F-NT2RP1001173

F-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds //8.1e-26:373:68//U79139

F-NT2RP1001185//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-32:388:73//AC006039

F-NT2RP1001199

F-NT2RP1001247//Homo sapiens signaling molecule LEFTY-A gene, exon 1.//2.0e-29:166:96//AF081508

F-NT2RP1001248//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//7.3e-50:128:99//AC002036

F-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//4.3e-91:344:93//AF029914

F-NT2RP1001286//Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's.//0.54:292:63//L44140

F-NT2RP1001294

F-NT2RP1001302

F-NT2RP1001310//Rabbit skeletal muscle mRNA for ryanodine receptor.//1.5e-07:335:64//X15750

F-NT2RP1001311//RPCI11-67014.TK RPCI11 Homo sapiens genomic clone R-67014, genomic survey sequence.//0.26:80:75//AQ239291

F-NT2RP1001313//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.//8.8e-75:304:98//AC004228

F-NT2RP1001361//*B. taurus* CI-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//2.7e-57:412:84//X68647

F-NT2RP1001385

F-NT2RP1001395//*Mus musculus* COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.4e-72:535:83//AF071316

F-NT2RP1001410//*Homo sapiens* DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//5.8e-105:570:94//AL021878

F-NT2RP1001424

F-NT2RP1001432

F-NT2RP1001449//*Homo sapiens* clone 24733 mRNA sequence.//1.7e-84:422:97//AF052149

F-NT2RP1001457//*Xenopus laevis* notchless (nle) mRNA, complete cds.//1.3e-47:471:73//AF069737

F-NT2RP1001466//HS\_3006\_A2\_D08\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3006 Col=16 Row=G, genomic survey sequence.//0.56:289:60//AQ154336

F-NT2RP1001475//*H. sapiens* genomic DNA fragment (clone NLMA194R).//0.0001  
1:91:79//Z95375

F-NT2RP1001482//*Mouse* oncogene (ect2) mRNA, complete cds.//4.0e-87:563:8  
5//L11316

F-NT2RP1001494

F-NT2RP1001543//*Drosophila melanogaster* DNA sequence (P1 DS01142 (D148)), complete sequence.//1.9e-27:387:67//AC004280

F-NT2RP1001546//*Homo sapiens* tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//8.0e-63:314:98//AF054840

F-NT2RP1001569//*Mus musculus* signal recognition particle receptor beta subunit mRNA, complete cds.//1.2e-68:514:81//U17343

F-NT2RP1001616//Human clone 23665 mRNA sequence.//7.6e-40:496:74//U90913

F-NT2RP1001665//CIT-HSP-2059N5.TF CIT-HSP Homo sapiens genomic clone 205  
9N5, genomic survey sequence.//2.4e-45:305:88//B69912

F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence./  
/1.5e-135:685:96//AF091081

F-NT2RP2000006//HS\_3061\_B2\_C03\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3061 Col=6 Row=F, genomic survey s  
equence.//1.9e-17:394:67//AQ178856

F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds.//3.5e-14:241:  
68//AB002390

F-NT2RP2000008//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 257E24, WORKING DRAFT SEQUENCE.//1.7e-34:147:99//AL034424

F-NT2RP2000027//Homo sapiens BAC clone RG118P15 from 8q21, complete sequ  
ence.//1.4e-32:345:75//AC005066

F-NT2RP2000032//F.rubripes GSS sequence, clone 060E22aG10, genomic surve  
y sequence.//5.0e-41:445:72//Z88655

F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//1.  
9e-76:383:97//AB018290

F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homol  
og (TID1) mRNA, complete cds.//2.4e-95:467:97//AF061749

F-NT2RP2000054//CIT-HSP-2328J24.TF CIT-HSP Homo sapiens genomic clone 23  
28J24, genomic survey sequence.//3.3e-39:236:91//AQ043092

F-NT2RP2000056//Rat mRNA for protein tyrosine phosphatase epsilon C, par  
tial cds.//3.2e-50:311:90//D78610

F-NT2RP2000067//Mus musculus DOC4 (Doc4) mRNA, complete cds.//3.0e-55:76  
6:66//AF059485

F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169),  
complete sequence.//2.0e-118:597:95//AC005754

F-NT2RP2000076//Homo sapiens clone NH0263G22, complete sequence.//0.0017

:423:60//AC006037

F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//2.1e-77:278:97//AF050079

F-NT2RP2000079//H.sapiens CpG island DNA genomic Mse1 fragment, clone 40 c2, forward read cpg40c2.ft1k.//3.2e-33:197:95//Z55440

F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//2.2e-158:752:98//AB018338

F-NT2RP2000091//HS\_2228\_A2\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=4 Row=C, genomic survey sequence.//0.26:55:90//AQ146363

F-NT2RP2000097

F-NT2RP2000098//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.5e-05:482:60//AC004961

F-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-22:274:69//AC003973

F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//4.9e-114:551:97//AB018356

F-NT2RP2000120//HS\_3000\_B1\_E03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=5 Row=J, genomic survey sequence.//1.8e-21:129:97//AQ090365

F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//4.2e-119:607:96//AF054177

F-NT2RP2000133//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.3e-07:339:63//AC004827

F-NT2RP2000147//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.0e-101:638:85//M62419

F-NT2RP2000153//Human DNA sequence from clone 218J18 on chromosome Xp11.3-11.4. Contains the NDP (Norrie Disease (Pseudoglioma)) gene and a CC1.3 Splicing Factor pseudogene. Contains ESTs, STSSs and GSSs, complete seq

uence.//0.45:377:58//AL034370

F-NT2RP2000157//*Homo sapiens* Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.0e-73:317:87//AC0059

24

F-NT2RP2000161//CIT-HSP-2353L5.TF.1 CIT-HSP *Homo sapiens* genomic clone 2 353L5, genomic survey sequence.//3.0e-14:123:90//AQ263431

F-NT2RP2000173

F-NT2RP2000175

F-NT2RP2000183//*F.rubripes* GSS sequence, clone 168M02aC2, genomic survey sequence.//3.7e-06:152:66//AL007295

F-NT2RP2000195//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//7.6e-62:170:99//AL023581

F-NT2RP2000205

F-NT2RP2000208//*Homo sapiens* chromosome 19, overlapping cosmids R29828 and F25496, complete sequence.//7.2e-80:170:90//AC003030

F-NT2RP2000224//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//5.5e-64:400:85//AC004382

F-NT2RP2000232//Human DNA sequence from PAC 196E23 on chromosome Xq26.1-27.2. Contains the TAT-SF1 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-3 (Uterine B ombesin Receptor, BRS-3) gene, an unknown gene coding for two isoforms, a predicted CpG island, ESTs and STSs.//2.2e-07:280:66//Z97632

F-NT2RP2000233//*Mus musculus* tumor metastasis associated gene product (M AG) mRNA, complete cds.//8.8e-30:508:67//U88401

F-NT2RP2000239//*Homo sapiens* chromosome 4 clone B353C18 map 4q25, complete sequence.//4.0e-79:504:87//AC004066

F-NT2RP2000248

F-NT2RP2000257//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*

\* from clone Y1E3, WORKING DRAFT SEQUENCE.//0.0078:286:60//AL021388

F-NT2RP2000258//CIT-HSP-2349P21.TF CIT-HSP Homo sapiens genomic clone 23  
49P21, genomic survey sequence.//5.7e-82:416:97//AQ059184

F-NT2RP2000270//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323),  
complete sequence.//4.5e-29:310:73//AC006116

F-NT2RP2000274

F-NT2RP2000283//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//6  
.3e-20:260:73//X74904

F-NT2RP2000288

F-NT2RP2000289

F-NT2RP2000297//Figure 2. Nucleotide and translated protein sequences of  
HPF1, -2, and -9.//4.6e-69:744:70//M27877

F-NT2RP2000298//Streptomyces coelicolor cosmid 2E9.//4.4e-05:502:59//AL0  
21530

F-NT2RP2000310//WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.1e-13:173  
:76//AC006082

F-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome  
1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehyd  
rogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF  
6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains  
ESTs and GSSs, complete sequence.//8.3e-144:731:95//AL022398

F-NT2RP2000328//Human DNA sequence from clone 931K24 on chromosome 20p12  
Contains ESTs and GSSs, complete sequence.//1.9e-102:555:90//AL034430

F-NT2RP2000329//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, co  
mplete cds.//6.4e-105:639:87//M25757

F-NT2RP2000337//HS\_2060\_B1\_E01\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2060 Col=1 Row=J, genomic survey s  
equence.//0.78:218:60//AQ243333

F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA,

complete cds.//3.6e-129:627:97//U83981

F-NT2RP2000369//HS\_2182\_B1\_B11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=21 Row=D, genomic survey sequence.//2.5e-87:421:99//AQ024835

F-NT2RP2000412//Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.72:170:65//AL021327

F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//5.0e-6 6:375:93//L28010

● F-NT2RP2000420//Homo sapiens full length insert cDNA YQ86E07.//9.2e-77:4 23:93//AF075093

F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//2.1e-126:609:96//AF102265

F-NT2RP2000438//CITBI-E1-2519019.TR CITBI-E1 Homo sapiens genomic clone 2519019, genomic survey sequence.//0.96:61:78//AQ276878

F-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//7.1e-17:341:67//AC004691

F-NT2RP2000459//H.sapiens mRNA for imogen 38.//5.7e-21:158:87//Z68747

● F-NT2RP2000498//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//3.2e-11:160:73//Z92844

F-NT2RP2000503//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//0.0031:187:66//AC005229

F-NT2RP2000510//Fugu rubripes GSS sequence, clone 066G04aC1, genomic survey sequence.//8.8e-07:179:64//AL026277

F-NT2RP2000516//Mus musculus t complex testis-specific protein (Tctex2) gene, wild type, promoter sequence.//0.19:72:81//U21671

F-NT2RP2000523//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//5.0e-115:570:96//AL022318

F-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds.//

/8.4e-37:196:98//AB005543

F-NT2RP2000617//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.81:354:60//AC005321

F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//1.3e-149:732:97//AB014514

F-NT2RP2000644//HS\_3211\_A1\_F06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3211 Col=11 Row=K, genomic survey sequence.//3.6e-42:282:86//AQ175486

F-NT2RP2000656

● F-NT2RP2000658//CITBI-E1-2518N15.TF CITBI-E1 Homo sapiens genomic clone 2518N15, genomic survey sequence.//0.57:141:66//AQ278386

F-NT2RP2000668

F-NT2RP2000678//Homo sapiens clone DJ0891L14, WORKING DRAFT SEQUENCE, 12 unordered pieces.//4.3e-22:433:62//AC004916

F-NT2RP2000704//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome System Human BAC Library) complete sequence.//2.7e-22:270:75//AC005913

F-NT2RP2000710//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3 ; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-32 :574:64//AC005122

● F-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//4.8e-113:546:98//AC004540

F-NT2RP2000731//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.97:115:70//AC004965

F-NT2RP2000758//Human LIM-kinasel and alternatively spliced LIM-kinasel (LIMK1) gene, complete cds.//9.7e-16:162:77//U62293

F-NT2RP2000764//HS\_2254\_B2\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=14 Row=H, genomic survey sequence.//0.071:45:95//AQ068887

F-NT2RP2000809

F-NT2RP2000812//*Egernia stokesii* clone EST3 microsatellite.//0.040:158:6

4//AF069698

F-NT2RP2000814

F-NT2RP2000816

F-NT2RP2000819

F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds.//1.1e-26:390

:70//AB002292

F-NT2RP2000842//*H.sapiens* mRNA for G protein-coupled receptor Edg-2.//1.  
2e-44:255:93//Y09479

F-NT2RP2000845

F-NT2RP2000863//Human partial cDNA sequence, clone x874; //5.9e-29:173:9  
4//Z47045

F-NT2RP2000880//*Homo sapiens* mRNA for KIAA0741 protein, complete cds.//2  
.4e-140:732:94//AB018284

F-NT2RP2000892

F-NT2RP2000931//*Homo sapiens* mRNA for KIAA0723 protein, complete cds.//3  
.4e-129:610:98//AB018266

F-NT2RP2000932//*Homo sapiens* BAC clone GS166A23 from 7p21, complete sequ  
ence.//1.8e-37:212:84//AC005014

F-NT2RP2000938//Human DNA sequence from cosmid RJ14 from a contig from t  
he tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Conta  
ins ESTs and CpG island.//1.6e-126:682:93//Z69890

F-NT2RP2000943//*Homo sapiens* mRNA for KIAA0755 protein, complete cds.//5  
.8e-112:533:98//AB018298

F-NT2RP2000965

F-NT2RP2000970//*Homo sapiens* DNA sequence from BAC 747E2 on chromosome 2  
2q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete  
sequence.//9.2e-101:505:96//AL021393

F-NT2RP2000985//*Homo sapiens* chromosome 17, clone hRPK.597\_M\_12, complet

e sequence.//1.6e-72:498:82//AC005277

F-NT2RP2000987//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//7.4e-12:171:77//AC002394

F-NT2RP2001036//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence.//1.2e-37:390:76//AC004167

F-NT2RP2001044//HS\_2253\_B1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=N, genomic survey sequence.//0.21:276:61//AQ069224

F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA 0488.//3.2e-144:696:97//AB007957

F-NT2RP2001065

F-NT2RP2001070//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//4.3e-104:775:81//U91561

F-NT2RP2001081//Rattus norvegicus synaptotagmin XI mRNA, complete cds.//3.7e-69:488:82//AF000423

F-NT2RP2001094//Human DNA sequence from PAC 410B11 on chromosome X contains STS.//7.4e-11:490:61//Z86063

F-NT2RP2001119//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745C22, WORKING DRAFT SEQUENCE.//5.1e-30:316:76//AL031596

F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds.//1.1e-31:519:63//D87072

F-NT2RP2001137//HS\_2193\_B2\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=24 Row=H, genomic survey sequence.//1.8e-11:136:78//AQ032187

F-NT2RP2001149//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete sequence.//6.2e-29:247:78//AC000076

F-NT2RP2001168//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated

to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LC B-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//0.23:207:66//AL009178

F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//2.3e-112:567:96//AB007949

F-NT2RP2001174//RPCI11-58L2.TK RPCI11 Homo sapiens genomic clone R-58L2, genomic survey sequence.//7.6e-07:196:64//AQ237306

F-NT2RP2001196

F-NT2RP2001218

F-NT2RP2001226//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//1.1e-09:320:65//U92893

F-NT2RP2001233//Human ZFP-36 mRNA for a zinc finger protein.//6.1e-71:681:72//X51760

F-NT2RP2001245//HS\_3062\_B1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=13 Row=L, genomic survey sequence.//1.5e-05:268:63//AQ143177

F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//2.5e-106:514:97//AB018353

F-NT2RP2001277//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//0.32:183:64//AE001430

F-NT2RP2001290//M. musculus mRNA for I47 clone.//8.6e-102:641:86//X61455

F-NT2RP2001295//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\* \* from clone Y105E8, WORKING DRAFT SEQUENCE.//0.20:171:63//AL022594

F-NT2RP2001312//Bovine synaptophysin mRNA, complete cds.//0.98:253:58//M22967

F-NT2RP2001327//Human B12 protein mRNA, complete cds.//5.8e-29:359:71//M80783

F-NT2RP2001328//CIT-HSP-2335A5.TF CIT-HSP Homo sapiens genomic clone 233

5A5, genomic survey sequence.//1.3e-65:366:94//AQ038539

F-NT2RP2001347//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.8e-31:325:77//AJ003147

F-NT2RP2001366//H.sapiens CpG island DNA genomic MseI fragment, clone 4e 11, forward read cpg4e11.fla.//1.7e-12:98:92//Z61305

F-NT2RP2001378//HS\_3054\_B2\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=6 Row=B, genomic survey sequence.//9.8e-17:131:89//AQ100721

● F-NT2RP2001381//Arabidopsis thaliana BAC T2L5.//0.080:434:59//AF096371

F-NT2RP2001392//S.pristinaespiralis snbC gene & snbDE gene.//0.019:267:59//Y11548

F-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//1.9e-16:133:78//Z93242

F-NT2RP2001397//Bos taurus cyclin B2 (CYCB2) mRNA, complete cds.//1.3e-63:419:84//AF080219

F-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds.//3.1e-98:747:79//U76759

● F-NT2RP2001423//Xenopus laevis ER1 mRNA, complete cds.//3.7e-34:269:85//AF015454

F-NT2RP2001427//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//3.2e-13:164:78//AC003065

F-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//3.0e-06:136:71//AF046702

F-NT2RP2001440//cDNA sequence coding for gamma protein.//7.9e-83:553:86//E02350

F-NT2RP2001445//P.falciparum complete gene map of plastid-like DNA (IR-A).//1.5e-09:829:57//X95275

F-NT2RP2001449//B.taurus mRNA for cleavage and polyadenylation specificity factor.//1.3e-136:766:90//X75931

F-NT2RP2001450

F-NT2RP2001467

F-NT2RP2001506//CIT-HSP-2374H21.TF CIT-HSP Homo sapiens genomic clone 23 74H21, genomic survey sequence.//7.9e-14:151:80//AQ109561

F-NT2RP2001511//Oryctolagus cuniculus translation initiation factor eIF2 C mRNA, complete cds.//2.6e-22:462:64//AF005355

F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARAL AR1.//2.0e-136:657:97//Y14494

F-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//1.2e-37:357:64//AC004596

F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//1.6e-103:384:94//AF035586

F-NT2RP2001560

F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA 0488.//4.4e-123:590:98//AB007957

F-NT2RP2001576//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.038:580:58//U32943

F-NT2RP2001581//Mus musculus semaphorin VIa mRNA, complete cds.//6.5e-09 :222:66//AF030430

F-NT2RP2001597//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//0.0057:361:60//U72648

F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//7.2e-137:647:98//AB018340

F-NT2RP2001613

F-NT2RP2001628//H.sapiens (xs128) mRNA, 380bp.//1.7e-15:279:68//Z36784

F-NT2RP2001634//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//5.4e-123:606:96//AF030233

F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds.//4.2e-144:687:97//AF058718

F-NT2RP2001663//H.sapiens mRNA for 2-phosphopyruvate-hydratase-alpha-enzyme.//1.0e-36:372:74//X84907

F-NT2RP2001675//S.pombe chromosome I cosmid c2G11.//0.070:507:59//Z54354

F-NT2RP2001677//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//2.0e-60:232:96//AC005259

F-NT2RP2001678//HS\_2007\_A2\_A04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2007 Col=8 Row=A, genomic survey sequence.//7.3e-62:370:91//AQ269699

F-NT2RP2001699//RPCI11-57B17.TK RPCI11 Homo sapiens genomic clone R-57B17, genomic survey sequence.//0.99:141:63//AQ115592

F-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//9.4e-117:604:95//AC004079

F-NT2RP2001721//Homo sapiens DNA sequence from clone 466I8 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//1.0:273:61//AL030998

F-NT2RP2001740//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete sequence.//1.0:356:62//AC000090

F-NT2RP2001748//Human mRNA for KIAA0003 gene, complete cds.//3.7e-18:151:86//D14697

F-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.0e-145:715:97//AC004783

F-NT2RP2001813//Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence.//0.38:340:60//AE001378

F-NT2RP2001839//HS\_3000\_B1\_C07\_MR CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.026:253:60//AQ090347

F-NT2RP2001861//Homo sapiens mRNA for paraplegin.//0.89:146:71//Y16610

F-NT2RP2001869//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0.040:174:62//AF027219

F-NT2RP2001876//Cyprinus carpio mRNA for allograft inflammatory factor-1, complete cds.//2.8e-44:483:71//AB012309

F-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.8e-87:496:92//AL031864

F-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//9.2e-112:633:90//M74161

F-NT2RP2001900//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\* \* from clone R08A5, WORKING DRAFT SEQUENCE.//0.0026:360:62//Z82281

F-NT2RP2001907//H.sapiens CpG island DNA genomic Mse1 fragment, clone 97 f11, forward read cpg97f11.ft1a.//4.2e-26:206:84//Z64125

F-NT2RP2001926//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.5e-06:621:59//AC004688

F-NT2RP2001936//cSRL-47D9-u cSRL flow sorted Chromosome 11 specific cosm id Homo sapiens genomic clone cSRL-47D9, genomic survey sequence.//3.1e-50:282:93//B04856

F-NT2RP2001943//Drosophila melanogaster cosmid 25E8.//0.00036:248:60//AL 009196

F-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.8e-7 8:232:99//AC005033

F-NT2RP2001947//Homo sapiens full length insert cDNA clone ZD81B04.//2.0 e-28:172:94//AF086442

F-NT2RP2001969//H.sapiens CpG island DNA genomic Mse1 fragment, clone 15  
2a8, reverse read cpg152a8.rtla.//1.0e-20:123:99//Z59378

F-NT2RP2001976

F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds.//0.  
0023:235:62//AB011117

F-NT2RP2001991//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//  
/3.1e-35:180:80//L22022

F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds.//9.  
8e-61:314:97//AB018299

● F-NT2RP2002032//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), co  
mplete sequence.//0.76:189:65//AC005895

F-NT2RP2002033//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2  
unordered pieces.//2.9e-12:160:79//AC004825

F-NT2RP2002041//Human BAC clone RG035E18 from 7q31, complete sequence.//  
0.0014:123:73//AC004029

F-NT2RP2002046//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human  
BAC library) complete sequence.//2.2e-86:722:77//AC004552

F-NT2RP2002047//Human DNA sequence from clone 21F7 on chromosome 6q16.1-  
21. Contains part of an exon of a putative new gene and STSs and GSSs, c  
omplete sequence.//0.13:350:61//AL033375

F-NT2RP2002058//S.cerevisiae chromosome XII reading frame ORF YLR129w.//  
9.7e-11:480:60//Z73301

F-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, co  
mplete cds.//6.5e-97:610:86//U87306

F-NT2RP2002070//beta -ADD=adducin beta subunit 63 kda isoform/membrane s  
keleton protein, beta -ADD=adducin beta subunit 63 kda isoform/membrane  
skeleton protein {alternatively spliced, exon 10 to 13 region} [human, G  
enomic, 1851 nt, segment 3 of 3].//0.0059:107:73//S81083

F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//1.0e-127:643:96

//AF052183

F-NT2RP2002078//F12016-T7.1 IGF Arabidopsis thaliana genomic clone F1201  
6, genomic survey sequence.//0.14:191:64//AQ249805

F-NT2RP2002079//Homo sapiens clone DJ0892G19, complete sequence.//0.0094  
:325:60//AC004917

F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//9.8  
e-111:533:97//AJ007509

F-NT2RP2002105//H.sapiens CpG island DNA genomic Mse1 fragment, clone 10  
h8, forward read cpg10h8.ft1a.//2.4e-29:178:94//Z58857

● F-NT2RP2002124//CIT-HSP-2023E9.TF CIT-HSP Homo sapiens genomic clone 202  
3E9, genomic survey sequence.//2.5e-32:202:92//B64468

F-NT2RP2002137//Human plasma membrane calcium ATPase (hPMCA4) mRNA, comp  
lete cds.//0.095:319:59//M25874

F-NT2RP2002154//Mus musculus mRNA for myosin, complete cds.//1.0:258:63/  
/D85923

F-NT2RP2002172//HS\_3020\_B1\_H02\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3020 Col=3 Row=P, genomic survey s  
equence.//1.2e-11:124:82//AQ093169

● F-NT2RP2002185//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B1  
5, genomic survey sequence.//2.8e-18:109:100//AQ201833

F-NT2RP2002192//Human PM-Scl-75 autoantigen (PM-scl) mRNA, complete cds.  
//2.7e-36:363:78//U09215

F-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein K  
ChAP mRNA, complete cds.//9.5e-82:477:89//AF032872

F-NT2RP2002208

F-NT2RP2002219//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from MAL4P1, WORKING DRAFT SEQUENCE.//1.0:378:58//AL034557

F-NT2RP2002231//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic  
sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.60:560:56//AC0

05308

F-NT2RP2002235//*P.falciparum* glutamic acid-rich protein gene, complete cds.//0.59:341:60//J03998

F-NT2RP2002252//*Mus musculus* mSin3A (sin3A) mRNA, complete cds.//3.5e-81:398:87//U22394

F-NT2RP2002256//*Homo sapiens* retinoic acid hydroxylase mRNA, complete cds.//6.6e-50:315:89//AF005418

F-NT2RP2002259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING DRAFT SEQUENCE.//9.7e-67:340:89//AL033527

F-NT2RP2002270//RPCI11-77C23.TV RPCI11 *Homo sapiens* genomic clone R-77C23, genomic survey sequence.//2.9e-18:79:93//AQ268098

F-NT2RP2002292//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING DRAFT SEQUENCE.//1.0:290:60//AL031033

F-NT2RP2002312//*Homo sapiens* CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.5e-93:467:96//AF069532

F-NT2RP2002316//HS\_2171\_B2\_D11\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2171 Col=22 Row=H, genomic survey sequence.//7.3e-94:463:97//AQ119673

F-NT2RP2002325//*Homo sapiens* mRNA for Pex11p, complete cds.//3.9e-123:64:95//AB015594

F-NT2RP2002333

F-NT2RP2002373//*F.rubripes* GSS sequence, clone 026F10aB8, genomic survey sequence.//0.46:234:61//Z87330

F-NT2RP2002385//*Homo sapiens* synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//9.4e-138:673:97//AF038958

F-NT2RP2002394//*P.falciparum* complete gene map of plastid-like DNA (IR-A).//0.79:421:56//X95275

F-NT2RP2002408//*F.rubripes* GSS sequence, clone 080G11aA8, genomic survey sequence.//5.7e-15:220:71//AL015615

F-NT2RP2002426//*Sus scrofa* SCAMP1 gene, exon 9.//7.1e-71:582:80//AJ22374

2

F-NT2RP2002439//*Caenorhabditis elegans* cosmid T07D3.//0.0018:210:67//AF0  
16682

F-NT2RP2002442//*Caenorhabditis elegans* cosmid T03F1.//2.8e-18:295:67//U8  
8169

F-NT2RP2002457//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-44M2, complete  
sequence.//1.9e-06:281:66//AC004381

F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds.//0.039:207:6  
3//D42045

F-NT2RP2002475

F-NT2RP2002479//*Homo sapiens* mRNA for ABC transporter 7 protein, complete  
cds.//2.4e-123:607:96//AB005289

F-NT2RP2002498//*Arabidopsis thaliana* BAC F3D13.//0.73:395:57//AF069300

F-NT2RP2002503//*Homo sapiens*, clone hRPK.15\_A\_1, complete sequence.//7.2  
e-18:134:90//AC006213

F-NT2RP2002504//*Homo sapiens* mRNA for KIAA0791 protein, complete cds.//1  
.2e-157:761:97//AB018334

F-NT2RP2002520

F-NT2RP2002537

F-NT2RP2002546//*Homo sapiens* Chromosome 11q12 pac pDJ741n15, WORKING DRA  
FT SEQUENCE, 7 unordered pieces.//0.83:252:60//AC004127

F-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing  
DNA polymerase gamma (polg) gene, complete sequence.//5.9e-93:186:99//AC  
005317

F-NT2RP2002591//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 54B20, WORKING DRAFT SEQUENCE.//4.0e-38:175:78//Z98304

F-NT2RP2002595//Sequence 2 from patent US 5763220.//1.5e-84:430:95//AR01  
2155

F-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//1.9e-43:28  
2:87//U19181

F-NT2RP2002609//Mus musculus defender against death 1 (DAD1) gene, parti  
al cds.//1.5e-11:99:90//AF051310

F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice va  
riant, 1316 bp.//5.6e-27:460:63//Y10806

F-NT2RP2002621

F-NT2RP2002643//Rat calmodulin III gene for calmodulin, promoter region  
and exon 1.//0.023:322:60//D90397

● F-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q2  
4.3-10q25.1, complete sequence.//3.9e-149:794:94//AC005384

F-NT2RP2002701//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 50024, WORKING DRAFT SEQUENCE.//9.2e-10:129:75//AL034380

F-NT2RP2002706//S.griseus secA gene.//1.3e-05:311:63//Y10980

F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2  
.5e-40:631:65//AB014572

F-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//4.8e-65:6  
00:73//AF041107

● F-NT2RP2002736//S.pombe chromosome II cosmid c887.//0.17:352:58//AL03338  
8

F-NT2RP2002740//Absidia glauca ORF, 3' end; (+) mating type surface prot  
ein (PSSP15) gene, complete cds; ORF, 5' end.//0.0073:274:66//M94861

F-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//7.5e  
-29:628:62//D89016

F-NT2RP2002750//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Sys  
tems Human BAC Library) complete sequence.//3.6e-31:568:67//AC005296

F-NT2RP2002752//Human BAC clone RG317M02 from 7p15-p21, complete sequenc  
e.//1.7e-08:206:63//AC002433

F-NT2RP2002753//Human DNA sequence from cosmid B11B7 on chromosome 22 co

ntains ESTs.//2.8e-71:195:89//Z82171

F-NT2RP2002769//*Streptomyces fradiae* tylactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//0.0016:412:60//U78289

F-NT2RP2002778//CIT-HSP-2059C5.TF CIT-HSP *Homo sapiens* genomic clone 205 9C5, genomic survey sequence.//6.8e-18:186:79//B69837

F-NT2RP2002800

F-NT2RP2002839//*Homo sapiens* Chromosome 11q12.2 PAC clone pDJ688p12 containing *uteroglobin* gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1 .2e-41:134:94//AC006078

● F-NT2RP2002857//Rat T-cell receptor active beta-chain V-region (V-beta6-J-beta2.5) mRNA, partial cds, clone TRB-4.//0.85:93:68//M18845

F-NT2RP2002862//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3084 Col=5 Row=0, genomic survey sequence.//5.0e-67:390:91//AQ186344

F-NT2RP2002880

F-NT2RP2002891//CIT-HSP-2310014.TF CIT-HSP *Homo sapiens* genomic clone 23 10014, genomic survey sequence.//0.11:53:90//AQ019792

F-NT2RP2002925//Pig mRNA for carbonyl reductase, complete cds.//0.66:194 :65//D16511

● F-NT2RP2002928//*Homo sapiens* pre-mRNA splicing factor (PRP17) mRNA, complete cds.//2.3e-135:628:99//AF038392

F-NT2RP2002929//*F. rubripes* GSS sequence, clone 123I23aA1, genomic survey sequence.//3.9e-06:66:83//AL017246

F-NT2RP2002939

F-NT2RP2002954

F-NT2RP2002959//*Mus musculus* ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//1.3e-47:411:79//U62483

F-NT2RP2002979//CIT-HSP-2340D12.TF CIT-HSP *Homo sapiens* genomic clone 23 40D12, genomic survey sequence.//4.6e-96:476:97//AQ057233

F-NT2RP2002980//Sequence 20 from Patent EP0705842.//4.0e-13:100:94//A522

30

F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.4e-09:272:61//AF059569

F-NT2RP2002987//Homo sapiens (subclone 6\_d9 from P1 H21) DNA sequence, complete sequence.//1.0e-22:293:67//AC000958

F-NT2RP2002993//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//4.0e-74:502:84//AF025424

F-NT2RP2003000//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-46:474:76//AC004765

F-NT2RP2003034//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//4.2e-23:202:82//AC005703

F-NT2RP2003073//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//3.4e-59:330:82//Z83822

F-NT2RP2003099//HS\_3008\_B2\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3008 Col=18 Row=F, genomic survey sequence.//1.4e-71:362:96//AQ089786

F-NT2RP2003108//Sequence 59 from patent US 5773577.//0.95:123:69//AR0143

62

F-NT2RP2003117//HS\_2034\_B2\_D12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=24 Row=H, genomic survey sequence.//1.5e-88:461:96//AQ230797

F-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//4.3e-46:470:72//AF079765

F-NT2RP2003125//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//5.7e-10:436:61//AC005329

F-NT2RP2003129//P. thunbergii cab gene.//0.00044:541:60//X61915

F-NT2RP2003137//CIT-HSP-2300J6.TR CIT-HSP Homo sapiens genomic clone 230 J6, genomic survey sequence.//5.0e-78:393:97//AQ012976

F-NT2RP2003157//Human DNA sequence from cDNA 16pHQG;16 from chromosome 1  
6p13.3.//5.4e-07:137:71//Z84716

F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//1.8e-111:581:93//D67025

F-NT2RP2003161//CITBI-E1-2506E20.TR CITBI-E1 Homo sapiens genomic clone  
2506E20, genomic survey sequence.//0.0025:156:67//AQ262657

F-NT2RP2003164

F-NT2RP2003165//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.4e-43:334:79//U91328

F-NT2RP2003177//Human signaling inositol polyphosphate 5 phosphatase SIP-110 mRNA, complete cds.//0.91:346:62//U50040

F-NT2RP2003194//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 996D20, WORKING DRAFT SEQUENCE.//1.7e-108:511:90//AL031597

F-NT2RP2003206

F-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//2.9e-136:726:93//X74794

F-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.6e-51:348:86//AF023657

F-NT2RP2003237//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//2.6e-56:415:83//AL031447

F-NT2RP2003243//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence.//2.1e-16:112:93//AQ047107

F-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//6.0e-114:696:87//L38481

F-NT2RP2003272//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey sequence.//3.8e-16:110:94//AQ201833

F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.5e-145:714:96//AB014525

F-NT2RP2003280//RPCI11-14I2.TVB RPCI-11 *Homo sapiens* genomic clone RPCI-11-14I2, genomic survey sequence.//6.4e-77:400:95//B85286

F-NT2RP2003286//CIT-HSP-2336D3.TF CIT-HSP *Homo sapiens* genomic clone 2336D3, genomic survey sequence.//5.3e-29:287:73//AQ041024

F-NT2RP2003293//*Homo sapiens* DNA from chromosome 19, BAC 33152, complete sequence.//1.5e-54:508:74//AC003973

F-NT2RP2003295//*Homo sapiens* RMP mRNA for RPB5 mediating protein, complete cds.//6.1e-85:416:97//AB006572

F-NT2RP2003297//*S.pombe* pho2 gene for specific p-nitrophenylphosphatase.//0.60:309:64//X62722

F-NT2RP2003307//*Mus musculus* kinesin light chain 2 (Klc2) mRNA, complete cds.//1.0e-45:442:75//AF055666

F-NT2RP2003308//*D.melanogaster* crn mRNA.//1.1e-63:697:70//X58374

F-NT2RP2003329//*Homo sapiens* chromosome 17, clone hCIT.131\_K\_11, complete sequence.//0.040:145:64//AC005288

F-NT2RP2003339

F-NT2RP2003347//*Plasmodium falciparum* MAL3P7, complete sequence.//0.12:275:60//AL034559

F-NT2RP2003367//*Homo sapiens* chromosome 4 clone B368A9 map 4q25, complete sequence.//0.83:225:63//AC005510

F-NT2RP2003391

F-NT2RP2003393//HS\_3218\_A2\_B09\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3218 Col=18 Row=C, genomic survey sequence.//0.021:93:79//AQ204356

F-NT2RP2003394

F-NT2RP2003401

F-NT2RP2003433//*Rattus rattus* sec61 homologue mRNA, complete cds.//4.2e-61:533:75//M96630

F-NT2RP2003445//*Homo sapiens* genomic DNA, chromosome 21q11.1, segment 1/

5, WORKING DRAFT SEQUENCE.//2.1e-49:301:72//AP000023

F-NT2RP2003446

F-NT2RP2003456//*Rickettsia prowazekii* strain Madrid E, complete genome;  
segment 3/4.//0.0018:366:60//AJ235272

F-NT2RP2003466//*Homo sapiens* chromosome 11, BAC CIT-HSP-311e8 (BC269730)  
containing the hFEN1 gene, complete sequence.//7.5e-16:189:68//AC004770

F-NT2RP2003480//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//  
1.9e-25:197:85//M21977

F-NT2RP2003499

2.1e-08:408:61//AB000826

F-NT2RP2003506//*Homo sapiens* clone NH0479C13, WORKING DRAFT SEQUENCE, 12  
unordered pieces.//1.9e-33:192:96//AC005236

F-NT2RP2003511//*Ceratopteris richardii* mRNA for CRHB11, partial cds.//1.  
0:328:60//AB013801

F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//7.3e-76:403:  
93//D87460

F-NT2RP2003517//Human osteosarcoma cell line U-2 OS mRNA fragment for PD  
GF-B chain (PDGF= platelet-derived growth factor).//1.5e-24:151:95//X037  
02

F-NT2RP2003522//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//  
1.3e-101:564:91//M21977

F-NT2RP2003533//Human DNA sequence from cosmid F1121 on chromosome 6.//2  
.0e-40:315:75//Z80899

F-NT2RP2003543

F-NT2RP2003559//*H.sapiens* CpG island DNA genomic Mse1 fragment, clone 90  
a5, reverse read cpg90a5.rt1a.//1.1e-20:122:99//Z56144

F-NT2RP2003564//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.  
//8.8e-27:664:63//M34551

F-NT2RP2003567//*Homo sapiens* mRNA for KIAA0462 protein, partial cds.//4.

1e-113:541:98//AB007931

F-NT2RP2003581

F-NT2RP2003596//*F.rubripes* GSS sequence, clone 036L10aF12, genomic survey sequence.//1.9e-11:210:65//AL012756

F-NT2RP2003604//*Homo sapiens* alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//1.9e-123:587:98//AF030233

F-NT2RP2003629

F-NT2RP2003643//*Mus musculus* mRNA for CMP-N-acetylneuraminic acid synthetase.//7.8e-88:582:84//AJ006215

F-NT2RP2003668//*Homo sapiens* clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//5.6e-47:335:83//AC005081

F-NT2RP2003687//*Homo sapiens* Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//1.2e-06:133:74//AC003684

F-NT2RP2003691//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 525L6, WORKING DRAFT SEQUENCE.//1.7e-47:337:81//AL023807

F-NT2RP2003702//*Rattus norvegicus* ovarian-specific protein mRNA, complete cds.//1.3e-65:458:82//U44803

F-NT2RP2003704//*H.sapiens* CpG island DNA genomic Mse1 fragment, clone 2a9, reverse read cpg2a9.rt1e.//3.8e-17:170:84//Z60615

F-NT2RP2003706//*Homo sapiens* mRNA for KIAA0525 protein, partial cds.//2.6e-108:518:98//AB011097

F-NT2RP2003713//HS\_2016\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2016 Col=9 Row=D, genomic survey sequence.//1.3e-11:102:90//AQ226895

F-NT2RP2003714//*Homo sapiens* DNA from chromosome 19, BAC 33152, complete sequence.//1.4e-27:249:78//AC003973

F-NT2RP2003727//RPCI11-77I19.TV RPCI11 *Homo sapiens* genomic clone R-77I19, genomic survey sequence.//3.4e-26:294:74//AQ268303

F-NT2RP2003737//*Homo sapiens* clone DJ1022I14, WORKING DRAFT SEQUENCE, 14

unordered pieces.//2.6e-74:194:91//AC004951

F-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-911E12,  
complete sequence.//1.7e-92:165:96//AC003964

F-NT2RP2003760//B.primitiveus mRNA for coat protein gamma-cop.//4.5e-76:  
696:73//X92987

F-NT2RP2003764//Homo sapiens gene for MTG16, exon 1b, partial sequence./  
/1.0:109:69//AB013275

F-NT2RP2003769

F-NT2RP2003770//Homo sapiens chromosome 17, clone hRPC.1050\_D\_4, comple  
te sequence.//3.0e-96:467:98//AC004771

F-NT2RP2003777

F-NT2RP2003781//tricarboxylate carrier [rats, liver, mRNA Partial, 2986  
nt].//7.2e-107:731:82//S70011

F-NT2RP2003793//CIT-HSP-2326L12.TF CIT-HSP Homo sapiens genomic clone 23  
26L12, genomic survey sequence.//7.0e-20:124:95//AQ038761

F-NT2RP2003825//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete  
sequence.//8.9e-06:151:74//AC004491

F-NT2RP2003840//Arabidopsis thaliana chromosome II BAC F12A24 genomic se  
quence, complete sequence.//0.018:145:69//AC005167

F-NT2RP2003857//HS\_3227\_A2\_G04\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3227 Col=8 Row=M, genomic survey s  
equence.//0.96:257:61//AQ303467

F-NT2RP2003859

F-NT2RP2003871//Homo sapiens 12q24 PAC RPCI1-74B13 (Roswell Park Cancer  
Institute Human PAC library) complete sequence.//2.0e-12:369:65//AC00237

5

F-NT2RP2003885//CITBI-E1-2514D6.TF CITBI-E1 Homo sapiens genomic clone 2  
514D6, genomic survey sequence.//0.13:167:64//AQ265722

F-NT2RP2003912//nek1=serine/threonine- and tyrosine-specific protein kin

ase [mice, erythroleukemia cells, mRNA, 4263 nt] .//1.3e-136:838:86//S458

28

F-NT2RP2003952

F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.1e-28:165:96//AB014458

F-NT2RP2003976//Human DNA sequence from clone 283E3 on chromosome 1p36.2 1-36.33. Contains the alternatively spliced gene for Matrix Metalloprote inase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cy cle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Prote in S7 pseudogene, part of the KIAA0447 gene, a novel alternatively splic ed gene similar to many (archae)bacterial, worm and yeast hypothetical g enes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.6e-24:298:74//AL0312

82

F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//9. 9e-160:783:96//AB018347

F-NT2RP2003984

F-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENC E, 11 unordered pieces.//1.7e-26:260:77//AC000382

F-NT2RP2003988//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c lone 862K6, WORKING DRAFT SEQUENCE.//9.1e-61:701:70//AL031681

F-NT2RP2004013//Human DNA sequence from clone 372K1 on chromosome 6q24 C ontains EST, STS, GSS and CpG Island, complete sequence.//3.0e-123:693:9 1//AL023580

F-NT2RP2004014

F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequ

ence.//5.8e-83:427:87//AC004780

F-NT2RP2004042

F-NT2RP2004066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 134019, WORKING DRAFT SEQUENCE.//5.6e-110:528:98//AL034555

F-NT2RP2004081

F-NT2RP2004098//HS\_2216\_A1\_B12\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2216 Col=23 Row=C, genomic survey  
sequence.//1.0e-07:86:84//AQ145694

F-NT2RP2004124//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey s  
equence.//3.0e-25:155:94//AQ136993

F-NT2RP2004142//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clon  
e: K8K14, complete sequence.//1.0:220:62//AB007645

F-NT2RP2004152//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)),  
complete sequence.//0.93:480:56//AC002493

F-NT2RP2004165//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 geno  
mic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.051:265:61  
//AC005140

F-NT2RP2004170//Homo sapiens distal-less homeobox protein (DLX7) gene, c  
omplete cds.//1.0:162:66//AF028235

F-NT2RP2004172//S. pombe chromosome II cosmid c24E9.//1.7e-06:466:59//AL0  
21816

F-NT2RP2004187//Homo sapiens full length insert cDNA YQ86E07.//3.5e-17:3  
54:64//AF075093

F-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//  
9.4e-53:397:82//AF003998

F-NT2RP2004196

F-NT2RP2004207//Human von Willebrand factor pseudogene corresponding to  
exons 23 through 34.//0.0023:386:61//M60676

F-NT2RP2004226//HS\_2186\_A1\_D03\_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2186 Col=5 Row=G, genomic survey sequence.//7.8e-58:370:87//AQ063813

F-NT2RP2004232//*H.sapiens* mRNA for protein kinase C mu.//1.2e-34:448:67//X75756

F-NT2RP2004239//*Homo sapiens* lck mRNA for protein kinase, complete cds.//5.2e-108:510:99//AB015718

F-NT2RP2004240//*Pyrococcus horikoshii* OT3 genomic DNA, 1166001-1485000 n t. position (6/7).//1.1e-12:489:61//AP000006

F-NT2RP2004242

F-NT2RP2004245

F-NT2RP2004270//*Streptomyces coelicolor* cosmid 1A9.//7.5e-07:462:62//AL0 34446

F-NT2RP2004300//*Homo sapiens* chromosome 19, cosmid R33632, complete sequence.//3.5e-11:299:64//AC005781

F-NT2RP2004316//*Homo sapiens* EXT-like protein 2 (EXTL2) mRNA, complete cds.//4.5e-150:735:97//AF000416

F-NT2RP2004321//*Drosophila melanogaster* DNA sequence (P1 DS02110 (D147)) , complete sequence.//0.98:267:59//AC004423

F-NT2RP2004339//Human Chromosome 16 BAC clone CIT987SK-A-355G7, complete sequence.//1.6e-40:419:75//AC002519

F-NT2RP2004347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.2e-72:439:82//AL031650

F-NT2RP2004364

F-NT2RP2004365

F-NT2RP2004366//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//0.92:427:57//AL031864

F-NT2RP2004373//*Homo sapiens* cosmid Qc15C1 and 94B6 from Xq28, complete sequence.//2.6e-26:493:65//AF035397

F-NT2RP2004389//HS\_2183\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//2.9e-11:83:96//AQ063969

F-NT2RP2004392

F-NT2RP2004396//*Homo sapiens* BAC clone RG135C18 from 7q21, complete sequence.//1.1e-171:875:95//AC005164

F-NT2RP2004399//*Homo sapiens* SYBL1 gene.//1.4e-24:467:64//AJ004799

● F-NT2RP2004400//*Arabidopsis thaliana* BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence.//0.00074:455:59//AF069441

F-NT2RP2004412//*H.sapiens* CpG island DNA genomic Mse1 fragment, clone 34g4, reverse read cpg34g4.rt1a.//5.0e-27:154:98//Z65369

F-NT2RP2004425

F-NT2RP2004463//*Streptomyces coelicolor* cosmid 2E9.//0.0053:196:65//AL021530

F-NT2RP2004476//*Drosophila melanogaster* cosmid 67A9.//5.2e-15:377:63//AL034388

● F-NT2RP2004490//*Homo sapiens* chromosome 16, P1 clone 94-10H (LANL), complete sequence.//4.3e-100:497:97//AC005591

F-NT2RP2004512//*Plasmodium falciparum* MAL3P5, complete sequence.//2.3e-07:815:57//AL034556

F-NT2RP2004523//*Homo sapiens* clone DJ0800G07, complete sequence.//8.5e-138:718:95//AC004890

F-NT2RP2004538//*Homo sapiens* mRNA for KIAA0591 protein, partial cds.//1.4e-137:687:96//AB011163

F-NT2RP2004551//CIT-HSP-2387G7.TF.1 CIT-HSP *Homo sapiens* genomic clone 2387G7, genomic survey sequence.//2.1e-85:484:91//AQ239555

F-NT2RP2004568//*H.vulgare* GAA-satellite DNA.//2.0e-07:292:62//Z50100

F-NT2RP2004580//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//4.5e-44:512:72//AL023755

F-NT2RP2004587//Candida albicans cytoskeleton assembly control protein (SLA2) gene, partial cds.//1.0:344:56//AF092908

F-NT2RP2004594//nbxb0019H13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0019H13r, genomic survey sequence.//0.053:324:60//AQ258020

F-NT2RP2004600

F-NT2RP2004602//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//0.12:109:73//AC005176

F-NT2RP2004614

F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//2.6e-102:49 6:98//AJ006291

F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.6e-153:728:98//AB007929

F-NT2RP2004675//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//0.092:239:61//AC005805

F-NT2RP2004681//Human DNA sequence from clone 51J23 on chromosome Xq26.3 -27.3. Contains an EST and GSSs, complete sequence.//1.0:236:61//AL03131 2

F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.3e-59:327:94//AB014525

F-NT2RP2004709//HS\_2033\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=8 Row=J, genomic survey sequence.//1.9e-15:187:74//AQ230714

F-NT2RP2004710//HS\_3185\_B2\_D07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=14 Row=H, genomic survey sequence.//9.9e-10:110:84//AQ172885

F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//6.4e-117:582:96//AB007947

F-NT2RP2004743//Human DNA sequence from PAC 37M17 chromosome X.//0.14:13

8:71//Z78022

F-NT2RP2004767//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65  
c11, reverse read cpg65c11.rt1a.//1.3e-24:217:81//Z62210

F-NT2RP2004768//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete  
cds.//1.6e-45:541:71//AF024636

F-NT2RP2004775//Plasmodium falciparum chromosome 2, section 35 of 73 of  
the complete sequence.//5.8e-13:697:59//AE001398

F-NT2RP2004791//Human HeLa mRNA isolated as a false positive in a two-hy  
brid-screen.//5.0e-53:353:84//U56252

F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta s  
ubunit (SCS) mRNA, partial cds.//1.5e-116:594:95//AF058953

F-NT2RP2004802

F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.1e  
-101:495:97//AF054179

F-NT2RP2004841//Human DNA sequence from cosmid J138017, between markers  
DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endoge  
nous retroviral like element.//7.6e-82:531:84//Z72519

F-NT2RP2004861//Fugu rubripes GSS sequence, clone 040017bA3, genomic sur  
vey sequence.//0.96:183:64//AL025645

F-NT2RP2004897//Human Chromosome X clone bWXD187, complete sequence.//4.  
8e-142:710:96//AC004383

F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//2.0e-82  
:418:95//AB007144

F-NT2RP2004936

F-NT2RP2004959//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey  
sequence.//3.5e-25:218:83//AQ150183

F-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1

(KS1) mRNA, complete cds.//2.5e-59:339:79//U56732

F-NT2RP2004962//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//3.6e-19:187:72//U91328

F-NT2RP2004967//Plasmodium falciparum MAL3P6, complete sequence.//0.0020:297:61//Z98551

F-NT2RP2004978//Chlamydomonas reinhardtii VSP-3 mRNA, complete cds.//0.22:162:69//L29029

● F-NT2RP2004982//F26D4-Sp6 IGF Arabidopsis thaliana genomic clone F26D4, genomic survey sequence.//0.13:273:61//B12642

F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds.//1.5e-20:431:65//D63478

F-NT2RP2004999

F-NT2RP2005000//R.rattus gene for beta-1 subunit of Na,K-ATPase.//0.019:240:63//X63375

F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//6.0e-159:782:97//AB014515

● F-NT2RP2005003//H.sapiens Staf50 mRNA.//3.1e-42:430:75//X82200

● F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//1.4e-98:501:96//AF100141

F-NT2RP2005018//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//1.0:209:63//AC004849

F-NT2RP2005020

F-NT2RP2005022//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-43:98:93//AC000380

F-NT2RP2005031//HS\_2052\_B2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=20 Row=N, genomic survey sequence.//0.019:363:61//AQ231464

F-NT2RP2005037//Human 3' of immunoglobulin heavy chain locus (IGHA2) gene //0.70:174:65//U64454

F-NT2RP2005038//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence //0.20:519:57//AC005696

F-NT2RP2005108

F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//2.0e-103:495:98//AB014564

F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//2.9e-27:157:98//X98743

● F-NT2RP2005139//Amycolatopsis mediterranei genes encoding rifamycin polyketide synthases, ORFs 1 to 5.//0.00024:547:59//AJ223012

● F-NT2RP2005140//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence //0.95:191:62//AC004527

F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.6e-89:447:96//AF045583

F-NT2RP2005147//HS\_3184\_A1\_E01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=1 Row=I, genomic survey sequence //0.10:294:60//AQ252226

● F-NT2RP2005159//H.sapiens CpG island DNA genomic Mse1 fragment, clone 132g6, forward read cpg132g6.ft1a.//1.1e-13:93:97//Z59162

F-NT2RP2005162//Caenorhabditis elegans cosmid F01F1.//2.6e-20:394:64//U13070

F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.4e-125:633:96//AJ007509

F-NT2RP2005204//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00016:316:60//U80808

F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence //0.51:52:92//AC005189

F-NT2RP2005239//S.pombe chromosome II cosmid c21D10.//1.3e-22:356:67//AL

031536

F-NT2RP2005254

F-NT2RP2005270//H.sapiens genomic DNA (chromosome 3; clone NL197R).//0.5

8:132:65//X87513

F-NT2RP2005276//Rat mRNA for brain acyl-CoA synthetase II, complete cds.

//9.0e-103:656:85//D30666

F-NT2RP2005287//Cavia porcellus zinc finger protein (zfoc1) mRNA, complete cds.//3.4e-37:302:84//L26335

F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.1e-122:604:96//AF060219

F-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//4.0e-140:670:98//AJ007590

F-NT2RP2005293//HS\_3245\_B1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=19 Row=J, genomic survey sequence.//8.2e-37:223:92//AQ217454

F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-95:483:96//AB014576

F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds.//8.2e-22:166:90//U11701

F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//0.39:353:62//AF032387

F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds.//8.8e-29:456:66//AB011138

F-NT2RP2005354//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//0.72:431:61//Z92844

F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//4.7e-99:489:96//AF072247

F-NT2RP2005360//Pan troglodytes huntingtin gene, partial exon.//0.93:105:67//L49358

F-NT2RP2005393//Rat parathyroid hormone receptor mRNA, complete cds.//2.

4e-08:97:83//M77184

F-NT2RP2005407

F-NT2RP2005436//Homo sapiens chromosome 16, cosmid clone 2H2 (LANL), complete sequence.//0.014:235:62//AC005346

F-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//4.0e-107:532:97//AQ055548

F-NT2RP2005453//F21C16TFC IGF Arabidopsis thaliana genomic clone F21C16, genomic survey sequence.//1.0:239:61//B97865

F-NT2RP2005457//B.taurus CI-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//4.7e-25:245:79//X68647

F-NT2RP2005464//Human DNA sequence from clone 836E8 on chromosome 20p12. Contains EST, CA repeat, STS, GSS, retroviral sequence, complete sequence.//4.6e-111:724:86//AL031679

F-NT2RP2005465//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//6.5e-18:152:75//AC006116

F-NT2RP2005472//Human DNA sequence from clone 1118D24 on chromosome 1p36.11-36.33. Contains part of a novel gene similar to worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal Protein L10 LIKE (pseudo)gene and two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2 (75 kD) (TNF Binding Protein 2, TBPII, TNF-R2, CD120B, TNFBR). Contains ESTs, STSs, GSSs, genomic marker D1S434 and a ca repeat polymorphism, complete sequence.//4.4e-12:89:97//AL031276

F-NT2RP2005476//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//4.3e-40:463:73//AC004130

F-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//3.2e-115:228:99//AC006030

F-NT2RP2005491//HS\_2253\_A2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=20 Row=M, genomic survey

sequence.//4.6e-23:234:80//AQ116847

F-NT2RP2005495

F-NT2RP2005496//HS\_3064\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=15 Row=K, genomic survey sequence.//5.3e-90:436:98//AQ143097

F-NT2RP2005498//Rabbit protein phosphatase 2A beta subunit mRNA, complete cds.//1.4e-63:503:78//M64931

F-NT2RP2005501//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10 q25, complete sequence.//0.86:183:63//AC005880

● F-NT2RP2005509//Homo sapiens cosmid LM1937 from Xq28.//1.0:160:65//U8269

5

F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//3.9e-81:444:92//AF092563

F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds.//6.9e-18:112:99//AB018307

F-NT2RP2005531//Human structural protein 4.1 mRNA, complete cds.//1.1e-06:282:60//M14993

F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.9e-153:747:97//AJ012449

● F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.9e-130:618:98//AB007963

F-NT2RP2005549//Mus musculus clone OST142, genomic survey sequence.//3.1e-43:277:89//AF046734

F-NT2RP2005555//HS\_2188\_A2\_D04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=8 Row=G, genomic survey sequence.//8.0e-05:195:65//AQ086723

F-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//2.5e-44:473:71//AF062529

F-NT2RP2005581//Homo sapiens BAC clone GS180J15 from 7q31, complete sequ

ence.//0.99:213:65//AC005016

F-NT2RP2005600//H.sapiens CpG island DNA genomic Mse1 fragment, clone 17  
2d12, reverse read cpg172d12.rt1a.//0.32:134:63//Z57359

F-NT2RP2005605

F-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//9.8e-91:447:9  
7//AF062085

F-NT2RP2005622

F-NT2RP2005635//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//8  
.6e-17:411:61//U10556

● F-NT2RP2005637//NATI (NATI\*10)=acetyltransferase 1 {3' region, polyadenylation polymorphism} [human, unrelated Caucasians, mRNA Partial Mutant, 300 nt].//0.22:156:65//S78829

F-NT2RP2005640//Mouse U6 RNA gene.//5.5e-19:249:76//X06980

F-NT2RP2005645//HS\_2201\_B2\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=14 Row=H, genomic survey sequence.//0.30:159:65//AQ066763

F-NT2RP2005651//H.sapiens DNA sequence.//0.00037:150:66//Z22493

F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds.//4.7e-07:351:62//AB006626

● F-NT2RP2005669//Homo sapiens KE05 protein mRNA, complete cds.//8.2e-98:4  
72:98//AF064605

F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//2.4e-94:462:98//AF089814

F-NT2RP2005683//HS-1024-B1-H05-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=9 Row=P, genomic survey sequence.//0.99:156:64//B34405

F-NT2RP2005690//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//7.7e-10:328:61//M77836

F-NT2RP2005694

F-NT2RP2005701//*Homo sapiens* 12p13.3 BAC RPCI11-288K12 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.72:160:65//AC0051

83

F-NT2RP2005712//*Homo sapiens* mRNA for KIAA0799 protein, partial cds.//1.6e-124:599:97//AB018342

F-NT2RP2005719//*R.norvegicus* mRNA for metallothionein-III.//0.86:117:64//X89603

F-NT2RP2005722//Human zinc finger protein ZNF136.//2.6e-44:415:77//U0936

7

F-NT2RP2005723//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//6.9e-15:153:81//AC002528

F-NT2RP2005726//*Homo sapiens* clone DJ0577P23, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.1e-41:138:95//AC005627

F-NT2RP2005732//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE.//0.61:303:60//Z93017

F-NT2RP2005741//*Homo sapiens* PALM gene, exon 1 and joined CDS.//0.52:116:67//Y16270

F-NT2RP2005748//Human Kox11 mRNA for zinc finger protein, partial.//0.11:136:66//X52342

F-NT2RP2005752//*Homo sapiens* TNFR-related death receptor-6 (DR6) mRNA, complete cds.//7.8e-22:134:96//AF068868

F-NT2RP2005753//*Homo sapiens* I-1 receptor candidate protein mRNA, complete cds.//1.2e-100:486:98//AF082516

F-NT2RP2005763//Human mRNA for KIAA0111 gene, complete cds.//0.00073:425:56//D21853

F-NT2RP2005767//*G.gallus* PB1 gene.//2.1e-73:544:80//X90849

F-NT2RP2005773//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//6.2e-15:153:82//M77836

F-NT2RP2005775//*Sus scrofa* mRNA for soluble angiotensin-binding protein,

complete cds.//1.2e-121:649:88//D11336

F-NT2RP2005781//*Pseudomonas aeruginosa* gene for MexX and MexY, complete  
cds.//0.96:184:60//AB015853

F-NT2RP2005784//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 1185N5, WORKING DRAFT SEQUENCE.//1.9e-63:222:96//AL034423

F-NT2RP2005804//*Oryza sativa* glycine-rich protein (OSGRP1) mRNA, comple  
te cds.//2.6e-07:232:64//AF010579

F-NT2RP2005812

F-NT2RP2005815//*Streptomyces* sp. gene for alkaline serine protease I.//0  
.031:358:59//X74103

F-NT2RP2005835//*Rattus norvegicus* mRNA for p47, complete cds.//2.5e-107:  
449:91//AB002086

F-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//  
5.1e-05:144:73//Z68873

F-NT2RP2005853//RPCI11-24D4.TKBF RPCI-11 *Homo sapiens* genomic clone RPCI  
-11-24D4, genomic survey sequence.//6.4e-13:130:85//AQ013490

F-NT2RP2005857//*Homo sapiens* chromosome-associated protein-C (hCAP-C) mR  
NA, partial cds.//1.7e-174:829:98//AF092564

F-NT2RP2005859//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 914P20, WORKING DRAFT SEQUENCE.//0.25:174:62//AL034553

F-NT2RP2005868//*Fugu rubripes* GSS sequence, clone 103I24aF4, genomic sur  
vey sequence.//7.8e-06:92:79//AL027276

F-NT2RP2005886//HS\_3187\_A2\_D08\_T7 CIT Approved Human Genomic Sperm Libra  
ry D *Homo sapiens* genomic clone Plate=3187 Col=16 Row=G, genomic survey  
sequence.//7.1e-95:494:95//AQ155885

F-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-32:660:6  
6//L11316

F-NT2RP2005901//*H.sapiens* CpG island DNA genomic Mse1 fragment, clone 15  
b5, reverse read cpg15b5.rt1a.//0.0026:66:84//Z54729

F-NT2RP2005908//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.4e-49:481:75//AC004241

F-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//6.6e-61:657:73//U63840

F-NT2RP2005942//H.sapiens PAP mRNA.//1.6e-46:618:67//X76770

F-NT2RP2005980//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//1.0e-48:533:71//AC005207

F-NT2RP2006023//HS\_3048\_A1\_A11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=21 Row=A, genomic survey sequence.//2.1e-25:167:91//AQ126553

F-NT2RP2006038//CIT-HSP-384K4.TR CIT-HSP Homo sapiens genomic clone 384K4, genomic survey sequence.//3.9e-06:102:74//B51912

F-NT2RP2006043//Human intercrine-alpha (hIRH) mRNA, complete cds.//1.9e-05:418:59//U19495

F-NT2RP2006052//Peromyscus polionotus ammobates dinucleotide microsatellite Ppa55.//0.0035:226:65//AF016861

F-NT2RP2006069//Human HepG2 partial cDNA, clone hmd3g02m5.//3.9e-11:121:85//D17047

F-NT2RP2006071

F-NT2RP2006098//Homo sapiens chromosome 21q22.2, cosmid D13C2, complete sequence.//0.46:264:59//AF027207

F-NT2RP2006100//Human Chromosome X, complete sequence.//3.2e-94:488:95//AC004073

F-NT2RP2006103//HS\_2254\_A2\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=4 Row=G, genomic survey sequence.//5.7e-27:156:96//AQ129602

F-NT2RP2006106//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.2e-62:655:71//AC000378

F-NT2RP2006141//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 537K23, WORKING DRAFT SEQUENCE.//1.2e-69:316:98//AL034405

F-NT2RP2006166//Homo sapiens chromosome 4 clone B32I8, complete sequence  
.//3.1e-45:387:81//AC004063

F-NT2RP2006184//Cricetulus griseus beta-1,6-N-acetylglucosaminyltransfer  
ase Lec4A cell line point mutant mRNA, complete cds.//0.99:111:73//U6258

7

F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.  
8e-113:567:96//AB014554

● F-NT2RP2006196//Homo sapiens clone DJ1189D06, complete sequence.//2.8e-2  
8:718:62//AC005232

F-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKIN  
G DRAFT SEQUENCE, 66 unordered pieces.//6.5e-83:239:94//AC006057

F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.4e-116:618:93//X964  
84

F-NT2RP2006237//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 230  
0P9, genomic survey sequence.//2.0e-18:118:97//AQ012480

● F-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA,  
complete cds.//7.6e-102:635:86//U49055

● F-NT2RP2006258//RPCI11-9N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11  
-9N9, genomic survey sequence.//8.6e-05:181:63//B71615

F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK./  
/0.44:111:71//X97630

F-NT2RP2006275//Pseudorabies virus UL[5,6,7,8,8.5,9,10,11,12,13] genes./  
/2.0e-05:501:59//X97257

F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.7e-138  
:679:97//AF035262

F-NT2RP2006320//P.falciparum pfmdr1 gene.//0.00013:425:60//X56851

F-NT2RP2006321//Homo sapiens DNA from chromosome 19, BAC 33152, complete

sequence.//4.1e-19:545:62//AC003973

F-NT2RP2006323//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745I14, WORKING DRAFT SEQUENCE.//8.9e-18:131:90//AL033532

F-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//6.2e-125:602:98//AC004893

F-NT2RP2006334//Homo sapiens chromosome 19, cosmid R27139, complete sequence.//2.1e-06:241:65//AC005514

F-NT2RP2006365//Fugu rubripes GSS sequence, clone 171K15aC5, genomic survey sequence.//7.8e-06:148:70//AL029590

● F-NT2RP2006393//Human DNA sequence from clone 80I19 on chromosome 6p21.3 1-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//6.8e-06:167:70//AL022727

F-NT2RP2006436//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//4.2e-92:363:84//AL023808

F-NT2RP2006441

F-NT2RP2006454//Sequence 8 from Patent W09517522.//2.9e-06:180:66//A4533

8

F-NT2RP2006456

● F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//3.4e-148:545:98//AJ006266

F-NT2RP2006467//Sus scrofa IgM heavy chain gene, switch region and exons encoding ch1-ch4 and secretion domains, partial cds.//0.061:201:66//U50149

F-NT2RP2006472

F-NT2RP2006534//Human DNA sequence from clone 272E8 on chromosome Xp22.1 3-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSSs, GSSs and a CA repeat polymorphism, complete sequence.//8.8e-10:273:66//Z93929

F-NT2RP2006554//Human DNA mismatch repair protein homolog (hMLH1) gene,

exon 6.//0.71:174:59//U40965

F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//6.6e-114:669:90//AF038966

F-NT2RP2006571//Rabbit cytochrome P-450 isozyme 2 (type B2) mRNA, complete cds, clone B2-1.//6.0e-26:503:63//M20855

F-NT2RP2006573//Molluscum contagiosum virus subtype 1, complete genome.//0.44:134:71//U60315

F-NT2RP2006598//Human BRCA2 region, mRNA sequence CG033.//5.0e-16:140:85//U50537

● F-NT2RP3000002//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//3.8e-32:214:89//U14571

F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.8e-136:637:98//AJ011972

F-NT2RP3000046//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//5.4e-05:571:60//L14320

F-NT2RP3000047

F-NT2RP3000050//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.0e-67:626:74//M27877

● F-NT2RP3000055//Genomic sequence from Human 9q34, complete sequence.//3.5e-10:394:64//AC001227

F-NT2RP3000068

F-NT2RP3000072//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence.//1.0:301:61//AC004746

F-NT2RP3000080//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE.//1.9e-44:297:79//AL021391

F-NT2RP3000085//Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase precursor mRNA, complete cds.//4.5e-33:528:65//U12536

F-NT2RP3000092//RPCI11-22M5.TV RPCI-11 Homo sapiens genomic clone RPCI-1-22M5, genomic survey sequence.//3.3e-27:157:97//B84237

F-NT2RP3000109//Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds.//0.92:185:64//L29260

F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.2e-112:286:89//AC005189

F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//9.0e-181:849:98//AB011164

F-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.264\_B\_14, complete sequence.//4.2e-24:155:94//AC005884

F-NT2RP3000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 500L14, WORKING DRAFT SEQUENCE.//7.2e-43:269:81//AL023583

F-NT2RP3000197//Homo sapiens interleukin 9 receptor (IL9R) pseudogene, exons 1-9.//0.098:405:57//L39063

F-NT2RP3000207//Drosophila melanogaster DNA sequence (P1 DS00164 (D269)), complete sequence.//0.96:608:55//AC004716

F-NT2RP3000220

F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.0e-18:509:58//AF059569

F-NT2RP3000235//Mouse Cosmid ma53a016 from 14D1-D2, complete sequence.//3.5e-05:224:65//AC004101

F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds.//2.1e-109:691:86//D86972

F-NT2RP3000251//Caenorhabditis elegans cosmid ZK930, complete sequence.//0.20:119:68//Z70213

F-NT2RP3000252//Homo sapiens cosmid 1F1, complete sequence.//9.8e-78:174:88//AF065393

F-NT2RP3000255

F-NT2RP3000267

F-NT2RP3000299//Mus musculus Crk-associated substrate (Cas-b) mRNA, complete cds.//5.9e-48:374:82//U48853

F-NT2RP3000312//Fruit fly (*D. melanogaster*) Glued mRNA, complete cds.//4.

9e-22:583:63//J02932

F-NT2RP3000320//RPCI11-36J1.TP RPCI-11 *Homo sapiens* genomic clone RPCI-1  
1-36J1, genomic survey sequence.//4.4e-06:87:88//AQ047107

F-NT2RP3000324//*Rattus norvegicus* potassium channel regulator 1 mRNA, co  
mplete cds.//5.5e-26:283:79//U78090

F-NT2RP3000333//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 973M2, WORKING DRAFT SEQUENCE.//1.0:309:60//AL033533

F-NT2RP3000341//*Homo sapiens* DNA sequence from PAC 95C20 on chromosome X  
p11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat poly  
morphisms, complete sequence.//6.7e-42:465:74//Z97181

F-NT2RP3000348

F-NT2RP3000350//*Homo sapiens* cosmid 1F1, complete sequence.//3.4e-79:174  
:88//AF065393

F-NT2RP3000359//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, co  
mplete cds.//2.2e-127:816:85//M25757

F-NT2RP3000361//*Schizosaccharomyces pombe* DNA for pre-mRNA splicing fact  
or, complete cds.//0.0075:288:58//D83743

F-NT2RP3000366//*Mus musculus* ras-related protein (rab18) mRNA, complete  
cds.//7.1e-134:693:94//L04966

F-NT2RP3000393//*Rattus norvegicus* mRNA for GABA-B R2 receptor.//0.049:30  
8:60//AJ011318

F-NT2RP3000397//*S.cerevisiae* chromosome VII reading frame ORF YGL120c.//  
0.00012:441:58//Z72642

F-NT2RP3000403//*Homo sapiens* formin binding protein 21 mRNA, complete cd  
s.//5.0e-174:841:97//AF071185

F-NT2RP3000418//*Homo sapiens* chromosome 17, clone hRPK.1053\_B\_8, comple  
te sequence.//7.9e-53:817:68//AC006083

F-NT2RP3000433//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 862K6, WORKING DRAFT SEQUENCE.//6.1e-31:590:63//AL031681

F-NT2RP3000439//Fugu rubripes GSS sequence, clone 075E22aB10, genomic survey sequence.//4.0e-19:169:81//AL026471

F-NT2RP3000441//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island.//2.4e-41:459:65//Z84488

F-NT2RP3000449//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.1e-100:365:87//AL031650

F-NT2RP3000451//HS\_2024\_A1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2024 Col=19 Row=1, genomic survey sequence.//0.011:367:57//AQ229420

F-NT2RP3000456//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//1.5e-89:458:96//AQ055548

F-NT2RP3000484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90L6, WORKING DRAFT SEQUENCE.//0.043:147:70//Z97353

F-NT2RP3000487//H.sapiens CpG island DNA genomic Mse1 fragment, clone 11b11, forward read cpg11b11.ft1a.//1.7e-11:96:92//Z64440

F-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//9.7e-17:109:97//X16667

F-NT2RP3000526//Homo sapiens full length insert cDNA clone YZ38E04.//4.1e-30:283:76//AF086071

F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds.//2.5e-34:706:63//D86966

F-NT2RP3000531//Mus musculus immunosuperfamily protein B12 mRNA, complete cds.//1.9e-14:220:70//AF061260

F-NT2RP3000542//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//0.00019:361:60//AC002554

F-NT2RP3000561//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//9.0e-171:827:98//AC006012

F-NT2RP3000562

F-NT2RP3000578//*F.rubripes* GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271

F-NT2RP3000582//CIT978SK-A-56H4.TP CIT978SK *Homo sapiens* genomic clone A-56H4, genomic survey sequence.//5.8e-07:239:66//B73597

F-NT2RP3000584

F-NT2RP3000590//*H.sapiens* CpG island DNA genomic Mse1 fragment, clone 170d7, forward read cpg170d7.ft1a.//3.0e-22:128:100//Z59723

F-NT2RP3000592//CIT-HSP-2288J7.TR CIT-HSP *Homo sapiens* genomic clone 228J7, genomic survey sequence.//2.2e-78:382:98//B98868

F-NT2RP3000596//CIT-HSP-2375J10.TR CIT-HSP *Homo sapiens* genomic clone 2375J10, genomic survey sequence.//0.00076:143:67//AQ109305

F-NT2RP3000599//*Caenorhabditis elegans* cosmid T19B10, complete sequence.//1.2e-13:295:66//Z74043

F-NT2RP3000603//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.37:520:57//L14320

F-NT2RP3000605//*Homo sapiens* chromosome 19, cosmid F20900, complete sequence.//8.8e-155:526:97//AC006128

F-NT2RP3000622//HS\_3213\_A2\_D02\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//4.1e-29:238:85//AQ175104

F-NT2RP3000624//*Homo sapiens* clone DJ0800G07, complete sequence.//0.47:75:80//AC004890

F-NT2RP3000628//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.//0.078:393:58//AL031313

F-NT2RP3000632//Human zinc finger protein zfp6 (ZF6) mRNA, partial cds.//1.4e-96:541:79//U71363

F-NT2RP3000644//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 un  
ordered pieces.//5.2e-46:421:77//AC005089

F-NT2RP3000661

F-NT2RP3000665//Human DNA sequence from clone 1191B2 on chromosome 22q13  
.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting  
killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an  
alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151; complete sequence.//1.7e-11:292:65//A

L022237

F-NT2RP3000685//H.sapiens mRNA for novel protein.//2.4e-80:460:92//X9996  
1

F-NT2RP3000690//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA1  
0F6.//1.0:141:65//Z77872

F-NT2RP3000736//Human mRNA for KIAA0140 gene, complete cds.//6.1e-20:127  
:96//D50930

F-NT2RP3000739//Rattus norvegicus golgi peripheral membrane protein p65  
(GRASP65) mRNA, complete cds.//1.1e-46:622:67//AF015264

F-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete  
cds.//4.7e-37:429:70//U16655

F-NT2RP3000753

F-NT2RP3000759//Caenorhabditis elegans cosmid Y57G11C, complete sequence  
.//2.8e-38:519:69//Z99281

F-NT2RP3000815//HS\_2237\_A2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=24 Row=G, genomic survey sequence.//0.79:151:61//AQ067252

F-NT2RP3000825//Campanula ramosa chloroplast NADH dehydrogenase (ndhF) gene, complete cds.//0.36:378:58//L39387

F-NT2RP3000826//Suid herpesvirus 1 Kaplan glycoprotein L (UL1) and uraci

l-DNA glycosylase (UL2) genes, complete cds, and (UL3) gene, partial cds  
//0.0025:291:62//U02513

F-NT2RP3000836//Mouse complement factor H-related protein mRNA, complete  
cds, clone 904.//0.69:563:57//M29009

F-NT2RP3000841//Human DNA sequence from PAC 121G13 on chromosome 6 conta  
ins flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repe  
at, CpG island, CpG island genomic fragments.//2.1e-46:666:68//Z86062

F-NT2RP3000845//Homo sapiens chromosome 19, cosmid R31237, complete sequ  
ence.//3.4e-92:193:93//AC005581

● F-NT2RP3000847//Human HepG2 3' region cDNA, clone hmd5d02.//3.4e-32:261:  
81//D16938

F-NT2RP3000850//Homo sapiens clone RG271G13, WORKING DRAFT SEQUENCE, 7 u  
nordered pieces.//5.1e-44:358:81//AC005082

● F-NT2RP3000852//Homo sapiens DNA sequence from PAC 117P20 on chromosome  
1q24. Contains the LNHR (SELL) gene coding for Lymph Node Homing Recepto  
r (L-Selectin precursor, LAM-1 Leukocyte Adhesion Molecule, Leukocyte su  
rface antigen Leu-8, TQ1, GP90-MEL, LECAM1 Leukocyte-Endothelial Cell Ad  
hesion Molecule 1, CD62L). Contains the SELE gene coding for E-Selectin  
precursor (CD62E, ELAM-1 Endothelial Leukocyte Adhesion Molecule 1, LECA  
M-2 Leukocyte-Endothelial Cell Adhesion Molecule 2). Contains an unknow  
n gene with homology to predicted yeast, plant and worm proteins. Contai  
ns ESTs and STSs, complete sequence.//4.4e-123:150:98//AL021940

F-NT2RP3000859//T19M2TF TAMU Arabidopsis thaliana genomic clone T19M2, g  
enomic survey sequence.//0.016:185:65//B60831

F-NT2RP3000865

F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain ho  
molog (Doc1) mRNA, complete cds.//2.0e-29:766:60//U53445

F-NT2RP3000869//H.sapiens gene for plectin.//1.1e-12:700:60//Z54367

F-NT2RP3000875//HS\_2236\_B1\_G10\_MF CIT Approved Human Genomic Sperm Libra

ry D *Homo sapiens* genomic clone Plate=2236 Col=19 Row=N, genomic survey sequence.//0.98:153:68//AQ154007

F-NT2RP3000901//Human herpesvirus 2 glycoprotein B precursor (UL27) gene, complete cds.//0.44:213:65//AF021340

F-NT2RP3000904//Rat  $\text{Na}^+$  channel mRNA, 3' end.//3.6e-106:505:99//M27223

F-NT2RP3000917//Mouse mRNA for Dhml protein, complete cds.//3.1e-132:691:93//D38517

F-NT2RP3000919//*Rattus norvegicus* golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//3.2e-97:585:88//AF015264

F-NT2RP3000968//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//5.8e-70:181:89//U91326

F-NT2RP3000980//*R.norvegicus* CYP3A1 gene, 5' flanking region.//6.1e-26:507:66//X98335

F-NT2RP3000994//HS-1049-B2-F03-MF.abi CIT Human Genomic Sperm Library C *Homo sapiens* genomic clone Plate=CT 771 Col=6 Row=L, genomic survey sequence.//1.5e-22:128:100//B39529

F-NT2RP3001004//*H.sapiens* CpG island DNA genomic Mse1 fragment, clone 39 c1, reverse read cpg39c1.rt1a.//5.9e-27:150:99//Z60925

F-NT2RP3001007//*Homo sapiens* clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.11:610:57//AC006039

F-NT2RP3001055//*Drosophila melanogaster*; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653

F-NT2RP3001057//*H.sapiens* HZF4 mRNA for zinc finger protein.//1.4e-49:437:77//X78927

F-NT2RP3001081//*Homo sapiens* RCC1-like G exchanging factor RLG mRNA, complete cds.//8.4e-50:534:74//AF060219

F-NT2RP3001084//*Homo sapiens* mRNA for KIAA0782 protein, partial cds.//1.2e-14:474:60//AB018325

F-NT2RP3001096//CIT-HSP-2305P8.TF CIT-HSP Homo sapiens genomic clone 230  
5P8, genomic survey sequence.//3.4e-37:222:93//AQ021278

F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds.//8.5e-33:712  
:64//D86969

F-NT2RP3001109//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing  
DNA polymerase gamma (polg) gene, complete sequence.//2.7e-116:186:99//A  
C005317

F-NT2RP3001111

F-NT2RP3001113//Human DNA sequence from cosmid U157D4, between markers D  
XS366 and DXS87 on chromosome X.//2.4e-05:702:58//Z68871

F-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete  
sequence.//1.9e-170:821:98//AC005189

F-NT2RP3001116//HS\_3075\_A1\_F01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=1 Row=K, genomic survey sequence.//7.3e-49:290:92//AQ120581

F-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-  
25.3 Contains exon from gene similar to 40S ribosomal protein, first cod  
ing exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequ  
ence.//1.4e-121:598:97//AL031864

F-NT2RP3001120//Human zinc finger protein ZNF136.//7.4e-76:687:75//U0936  
7

F-NT2RP3001126//Bovine herpesvirus type 1 DNA for UL36, UL37, UL38, UL39  
, UL40 and UL41.//6.8e-05:344:64//Z49078

F-NT2RP3001133//Nephila clavipes minor ampullate silk protein MiSp1 mRNA  
, partial cds.//0.00021:529:60//AF027735

F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//3.  
6e-179:851:98//AB018305

F-NT2RP3001147//RPCI11-3M16.TP RPCI-11 Homo sapiens genomic clone RPCI-1  
1-3M16, genomic survey sequence.//2.1e-15:106:96//B48859

F-NT2RP3001150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//2.0e-159:418:95//AL034379

F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//5.1e-190:891:98//AJ006266

F-NT2RP3001176//Human DNA sequence from clone 879K22 on chromosome 1q32.

1-41 Contains GSS, complete sequence.//1.1e-69:207:97//AL034351

F-NT2RP3001214//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.16:475:58//AC005507

● F-NT2RP3001216//Homo sapiens clone DJ0635005, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-05:561:56//AC004845

F-NT2RP3001221

F-NT2RP3001232//Mouse mRNA for serine protease PC6, complete cds.//1.0e-1 1:120:87//D12619

F-NT2RP3001236

F-NT2RP3001239//Mouse MAP1B mRNA for MAP1B microtubule-associated protein.//3.9e-19:501:61//X51396

● F-NT2RP3001245//CITBI-E1-2505C1.TF.1 CITBI-E1 Homo sapiens genomic clone 2505C1, genomic survey sequence.//8.5e-70:337:100//AQ242007

● F-NT2RP3001253//CITBI-E1-2505N14.TR CITBI-E1 Homo sapiens genomic clone 2505N14, genomic survey sequence.//0.83:235:60//AQ260430

F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds.//3.8e-47:761:64//AB018269

F-NT2RP3001268//Homo sapiens zinc finger protein (HZF6) mRNA, 5' UTR and partial cds.//2.3e-64:618:72//AF027513

F-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//2.6e-99:669:83//Y18101

F-NT2RP3001274//Human ABL gene, exon 1b and intron 1b, and putative M860 4 Met protein (M8604 Met) gene, complete cds.//0.99:400:58//U07561

F-NT2RP3001281//*Homo sapiens* chromosome 17, clone hRPK.318\_A\_15, complete sequence.//5.9e-39:304:70//AC005837

F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds.//7.6e-47:544:69//D87457

F-NT2RP3001307//*Ambystoma tigrinum* RPE65 protein mRNA, complete cds.//2.4e-27:547:63//AF047465

F-NT2RP3001318//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00022:624:60//AC004709

● F-NT2RP3001325//*Caenorhabditis elegans* cosmid F36H12.//0.25:523:59//AF078790

F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds.//5.1e-29:345:73//D86966

F-NT2RP3001339//*Rattus norvegicus* mytonic dystrophy kinase-related Cdc42-binding kinase (MRCK) mRNA, complete cds.//1.2e-151:821:91//AF021935

F-NT2RP3001340//*Homo sapiens* HMG box factor SOX-13 mRNA, complete cds.//5.3e-27:247:81//AF083105

● F-NT2RP3001355//*Homo sapiens* Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-16:130:76//AC000052

F-NT2RP3001356

F-NT2RP3001374

F-NT2RP3001383//*Homo sapiens* DNA sequence from PAC 140C12 on chromosome 6q26-q27.//0.00082:365:61//AL008628

F-NT2RP3001384//*Homo sapiens* HRIHFB2018 mRNA, partial cds.//6.4e-157:743:98//AB015332

F-NT2RP3001392//Human DNA sequence from PAC 302D9 on chromosome 22q11.2-pter. Contains STS, complete sequence.//0.045:359:61//Z82198

F-NT2RP3001396//*Drosophila melanogaster* DNA sequence (P1 DS08860 (D181))

, complete sequence.//1.3e-16:336:65//AC004296

F-NT2RP3001398//*Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.*//3.1e-100:711:82//U49046

F-NT2RP3001399//*Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.*//5.4e-20:245:73//AC005521

F-NT2RP3001407//*RPCI11-41A20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41A20, genomic survey sequence.*//0.051:306:59//AQ029031

F-NT2RP3001420//*Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.*//0.90:170:65//AL021327

F-NT2RP3001426//*Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.*//2.9e-89:138:98//AL031447

F-NT2RP3001427//*CIT-HSP-2302H24.TF CIT-HSP Homo sapiens genomic clone 2302H24, genomic survey sequence.*//8.1e-36:212:94//AQ020997

F-NT2RP3001428//*Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.*//8.5e-73:431:91//U69668

F-NT2RP3001432//*HS\_3032\_B1\_A03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=5 Row=B, genomic survey sequence.*//0.00024:111:76//AQ096619

F-NT2RP3001447

F-NT2RP3001449//*Human DNA sequence from clone 283E3 on chromosome 1p36.2-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae)bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein)*

n), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.1e-105:223:99//AL031

282

F-NT2RP3001453//Ralstonia sp. E2 positive phenol-degradative gene regulator (poxR), phenol hydroxylase components (poxA, poxB, poxC, poxD, poxE, poxF), and ferredoxin-like protein (poxG) genes, complete cds.//0.75:34

9:59//AF026065

F-NT2RP3001457

F-NT2RP3001459

● F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds.//1.3e-08:168:70//AF072836

F-NT2RP3001490

F-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//1.0e-26:191:90//U13395

F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//8.5e-171:804:98//AF064801

F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete cds.//8.9e-140:743:91//U36499

● F-NT2RP3001529//Streptomyces griseus DNA for ribosoma protein L21, ribosomal protein L27, Obg, complete cds.//2.1e-14:517:59//D87916

F-NT2RP3001538//Capra hircus hircus clone 12 RAPD PCR sequence, genomic survey sequence.//4.7e-05:217:63//AF078176

F-NT2RP3001554//Rattus norvegicus microtubule-associated protein 1A MAP1A (Mtap-1) mRNA, complete cds.//4.3e-17:332:67//M83196

F-NT2RP3001580//RPCI11-91E19.TV RPCI11 Homo sapiens genomic clone R-91E19, genomic survey sequence.//4.2e-15:110:91//AQ281332

F-NT2RP3001587//S.pombe chromosome II cosmid c16H5.//6.6e-28:491:64//AL022104

F-NT2RP3001589//RPCI11-68M15.TK RPCI11 Homo sapiens genomic clone R-68M1

5, genomic survey sequence.//8.7e-108:517:98//AQ237629

F-NT2RP3001607//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human B  
AC library) complete sequence.//1.0e-09:257:65//AC004674

F-NT2RP3001608//Methylococcus capsulatus methane monooxygenase component  
A alpha chain, methane monooxygenase A beta chain and methane monooxyge  
nase component C genes, complete cds.//0.59:450:57//M90050

F-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21.3  
1-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory recep  
tor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, c  
omplete sequence.//1.8e-42:278:79//AL021808

F-NT2RP3001629

F-NT2RP3001634//Homo sapiens mRNA for Ariadne-2 protein.//1.5e-63:276:97  
//AJ130978

F-NT2RP3001642//Caenorhabditis elegans cosmid F45E6, complete sequence./  
/0.018:127:66//Z68117

F-NT2RP3001646

F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.4  
e-171:816:98//AJ012449

F-NT2RP3001672//Drosophila melanogaster transcriptional repressor protei  
n (Scm) mRNA, complete cds.//1.6e-38:542:66//U49793

F-NT2RP3001676//HS\_3090\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3090 Col=7 Row=D, genomic survey s  
equence.//3.1e-07:333:64//AQ123250

F-NT2RP3001678//Drosophila melanogaster; Chromosome 3L; Region 63C5-63D3  
; P1 clone DS01859, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.0:539  
:57//AC004358

F-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of  
hepatocellular colorectal and non-small cell lung cancer , segment 3/11.  
//2.8e-130:355:96//AB020860

F-NT2RP3001688//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//2.1e-37:512:70//AF059273

F-NT2RP3001690//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 230P9, genomic survey sequence.//2.8e-19:123:95//AQ012480

F-NT2RP3001698//Rat mRNA for RhoGAP, complete cds.//9.4e-11:167:74//D31962

F-NT2RP3001708//H.sapiens CpG island DNA genomic Mse1 fragment, clone 4g7, reverse read cpg4g7.rt1d.//1.3e-17:113:97//Z61312

F-NT2RP3001712//M.musculus mRNA for HP1-BP74 protein.//2.2e-95:601:88//X99642

F-NT2RP3001716

F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.4e-159:565:97//AF054177

F-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.//1.7e-132:786:88//AF008554

F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds.//3.9e-104:811:78//D50918

F-NT2RP3001739//Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGR Region, complete sequence.//6.5e-07:178:69//AC000097

F-NT2RP3001752//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//5.2e-31:311:77//AL031311

F-NT2RP3001753//Sequence 29 from patent US 5658882.//0.11:513:58//I62381

F-NT2RP3001764//Sequence 6 from Patent WO9706245.//6.4e-47:673:66//A59888

8

F-NT2RP3001777//Caenorhabditis elegans cosmid T10E10.//0.078:290:63//U39644

F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//2.8e-151:710:98//AB007928

F-NT2RP3001792//*Mus musculus* myelin gene expression factor (MEF-2) mRNA, partial cds.//1.2e-26:213:85//U13262

F-NT2RP3001799//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//8.4e-51:168:95//AL031284

F-NT2RP3001819//*S. glaucescens* genes strU, strX, strV and strW for 5'-hydroxystreptomycin pruduction and transport polypeptides.//0.084:526:58//X89010

F-NT2RP3001844//HS\_3110\_B1\_E10\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3110 Col=19 Row=J, genomic survey sequence.//1.5e-40:232:82//AQ140433

F-NT2RP3001854//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.14:452:58//AC005505

F-NT2RP3001855//*Mus musculus* homeobox protein PKNOX1 (Pknox1) mRNA, complete cds.//2.7e-39:575:67//AF061270

F-NT2RP3001857//*M. musculus* tex292 mRNA (5' region).//8.7e-07:106:81//X80434

F-NT2RP3001896

F-NT2RP3001898//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 163G9, WORKING DRAFT SEQUENCE.//0.094:456:60//AL008733

F-NT2RP3001915//*Caenorhabditis elegans* cosmid C12D8, complete sequence.//0.58:482:56//Z73969

F-NT2RP3001926//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.42:401:58//AL034557

F-NT2RP3001929//*Homo sapiens* chromosome 16, cosmid clone RT102 (LANL), complete sequence.//3.1e-28:263:77//AC004651

F-NT2RP3001931

F-NT2RP3001938//CIT-HSP-2165E8.TR CIT-HSP *Homo sapiens* genomic clone 2165E8, genomic survey sequence.//3.6e-24:182:91//B95475

F-NT2RP3001943//*Homo sapiens* mRNA for KIAA0675 protein, complete cds.//1

.8e-165:815:96//AB014575

F-NT2RP3001944

F-NT2RP3001969//*Homo sapiens* chromosome 12p13.3 clone RPCI11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//4.8e-62:304:89//AC005844

F-NT2RP3001989//*Plasmodium falciparum* strain Dd2 heat shock protein 86 (HSP86), 01 (o1), 03 (o3), 02 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//8.2e-10:564:60//AF030694

F-NT2RP3002002//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//2.5e-57:361:80//Z83822

F-NT2RP3002004//Sequence 3 from patent US 5798245.//1.6e-26:104:100//AR025386

F-NT2RP3002007//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the P rader-Willi/Angelman Syndrome region, complete sequence.//0.0053:633:58//AC004137

F-NT2RP3002014//*Drosophila melanogaster* DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence.//1.3e-32:334:68//AC004640

F-NT2RP3002033//*H.sapiens* DNA sequence.//0.012:214:63//Z22493

F-NT2RP3002045//Rat mRNA for alpha-c large chain of the protein complex AP-2 associated with clathrin.//8.7e-116:713:86//X53773

F-NT2RP3002054//*Mycobacterium tuberculosis* H37Rv complete genome; segment 143/162.//1.6e-12:613:60//AL021841

F-NT2RP3002056//Human DNA sequence from PAC 358H7 on chromosome X.//0.17:566:59//Z77249

F-NT2RP3002057//*Homo sapiens* clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//3.3e-24:167:82//AC005682

F-NT2RP3002062

F-NT2RP3002063//*Rickettsia prowazekii* strain Madrid E, complete genome;

segment 3/4.//0.24:508:58//AJ235272

F-NT2RP3002081//HS\_2001\_B1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//9.7e-22:155:90//AQ218494

F-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//9.6e-66:562:77//AC006210

F-NT2RP3002102//CIT-HSP-2307B10.TR CIT-HSP Homo sapiens genomic clone 23 07B10, genomic survey sequence.//5.9e-16:214:74//AQ018040

F-NT2RP3002108

F-NT2RP3002142//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.6e-29:414:68//AC004020

F-NT2RP3002146//Pseudomonas fluorescens polyketide synthase type I (pltB) and polyketide synthase type I (pltC) genes, complete cds.//0.96:434:6 0//AF003370

F-NT2RP3002147//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329F2, WORKING DRAFT SEQUENCE.//1.3e-63:380:91//AL031710

F-NT2RP3002151//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//9.9e-60:315:80//U95742

F-NT2RP3002163

F-NT2RP3002165//M.musculus HCNGP mRNA.//1.4e-142:867:87//X68061

F-NT2RP3002166//Homo sapiens chromosome X, clone hcIT.200\_L\_4, complete sequence.//0.090:394:59//AC006121

F-NT2RP3002173//HS\_3062\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=9 Row=N, genomic survey sequence.//3.3e-101:509:96//AQ193219

F-NT2RP3002181//Human DNA sequence from clone 24o18 on chromosome 6p21.3 1-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//4.5e-106:432:84//AL021808

F-NT2RP3002244//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.63:353:60//AC005321

F-NT2RP3002248//HS\_3029\_A1\_D10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3029 Col=19 Row=G, genomic survey sequence.//3.5e-10:125:79//AQ094880

F-NT2RP3002255//Bovine herpesvirus type 1 immediate-early transcriptional control protein (BICP4) gene, 5' end.//5.6e-09:629:59//L14321

F-NT2RP3002273//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence.//4.9e-35:366:74//B03004

F-NT2RP3002276//B.taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex.//0.023:326:60//X64898

F-NT2RP3002303//Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome.//3.8e-12:643:57//AE000810

F-NT2RP3002304//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-09:490:60//AC005504

F-NT2RP3002330//Human DNA sequence from cosmid L58b6, Huntington's Disease Region, chromosome 4p16.3, containing STS matches.//1.9e-93:572:88//Z49862

F-NT2RP3002343//HS\_3010\_A2\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3010 Col=16 Row=C, genomic survey sequence.//9.0e-75:373:97//AQ119068

F-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.9e-64:588:75//X16396

F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene, alternatively spliced form.//1.3e-164:770:98//Y16355

F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds.//1.

4e-190:911:98//AB018331

F-NT2RP3002399

F-NT2RP3002402//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//7.2e-25:249:79//D89340

F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//1.2e-138:649:99//AB014578

F-NT2RP3002484//CIT-HSP-367N3.TP.1 CIT-HSP Homo sapiens genomic clone 367N3, genomic survey sequence.//5.0e-18:115:96//B78927

F-NT2RP3002501//Caenorhabditis elegans cosmid K01C8, complete sequence./0.00020:170:65//Z49068

F-NT2RP3002512//Homo sapiens clone 664 unknown mRNA, partial sequence.//1.6e-59:308:97//AF091088

F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds.//1.4e-144:763:93//U35246

F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//1.8e-178:833:98//AB018272

F-NT2RP3002549//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-26:123:72//AC004821

F-NT2RP3002566//Streptomyces viridifaciens sigma factor (hrdD) gene, complete cds.//0.76:459:59//U60418

F-NT2RP3002587//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//4.6e-13:199:76//AC004617

F-NT2RP3002590//Porphyra purpurea chloroplast, complete genome.//0.88:284:60//U38804

F-NT2RP3002602//CIT978SK-A-441H11-2.TPB CIT978SK Homo sapiens genomic clone A-441H11, genomic survey sequence.//2.0e-22:140:95//B68331

F-NT2RP3002603

F-NT2RP3002628//C.acetobutylicum dnaJ and orfB genes.//2.0e-05:333:60//X69050

F-NT2RP3002631

F-NT2RP3002650//*Mus musculus* mRNA for cartilage-associated protein (CASP)  
).//1.5e-20:641:62//AJ006469

F-NT2RP3002659//*Bovine herpesvirus type 1* UL22-35 genes././/5.2e-05:621:59  
//Z78205

F-NT2RP3002660//*Homo sapiens* PAC clone DJ1006K12 from 7q31.2-q31, complete  
sequence././/0.98:453:57//AC004946

F-NT2RP3002663//*Homo sapiens* chromosome 19, cosmid F6697, complete seque  
nce././/3.3e-22:407:67//AC006129

F-NT2RP3002671//*S.pombe* chromosome III cosmid c553././/1.0e-12:336:66//AL0  
23704

F-NT2RP3002682//*Caenorhabditis elegans* cosmid F17C11, complete sequence.  
//1.3e-21:448:64//Z72507

F-NT2RP3002687//CIT978SK-A-789B1.TP CIT978SK *Homo sapiens* genomic clone  
A-789B1, genomic survey sequence././/2.5e-25:173:91//B51656

F-NT2RP3002688//*Mouse* mRNA for kinesin-like protein (Kif1b), complete cd  
s././/1.2e-73:728:74//D17577

F-NT2RP3002701//CITBI-E1-2507L14.TF CITBI-E1 *Homo sapiens* genomic clone  
2507L14, genomic survey sequence././/0.0012:55:92//AQ263530

F-NT2RP3002713

F-NT2RP3002763//*Caenorhabditis elegans* cosmid T20F10, complete sequence.  
//0.98:209:63//Z81594

F-NT2RP3002770

F-NT2RP3002785//*Homo sapiens* laminin beta-4 chain precursor (LAMB4) mRNA  
, alternatively spliced short variant, partial cds././/0.78:515:57//AF0293  
25

F-NT2RP3002799//Human DNA sequence from clone 1052M9 on chromosome Xq25.  
Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (1  
ymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal prot

ein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//1.9e-21:167:79//AL022718

F-NT2RP3002810//Homo sapiens chromosome 17, clone hRPK.215\_E\_13, complete sequence.//0.32:187:66//AC005549

F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds.//6.9e-54:615:70//AF004715

F-NT2RP3002861//Caenorhabditis elegans cosmid M03F4.//4.2e-05:226:65//U64601

F-NT2RP3002869//Mus musculus semaphorin VIA mRNA, complete cds.//2.0e-93:638:83//AF030430

F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds.//8.5e-89:557:8//AB001895

F-NT2RP3002877//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE, 100 unordered pieces.//7.9e-12:160:78//AC006087

F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//5.7e-180:853:98//AB018314

F-NT2RP3002911//RPCI11-24N15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-24N15, genomic survey sequence.//2.3e-13:442:61//B88815

F-NT2RP3002948//, complete sequence.//2.2e-110:637:91//AC005500

F-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.7e-166:793:98//AC005754

F-NT2RP3002955//Human HepG2 partial cDNA, clone hmd3c02m5.//0.00011:61:95//D17024

F-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.2e-128:808:85//D30666

F-NT2RP3002972//H.sapiens (xs168) mRNA, 381bp.//1.5e-43:312:85//Z36820

F-NT2RP3002978//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00044:527:57//AC005505

F-NT2RP3002985//Genomic sequence from Human 9q34, complete sequence.//0.

92:341:60//AC001644

F-NT2RP3002988//HS\_3015\_A1\_B07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=13 Row=C, genomic survey sequence.//4.4e-05:379:58//AQ091708

F-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.4e-72:197:79//AF109905

● F-NT2RP3003032//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-80, complete sequence.//1.6e-08:809:58//AL010153

F-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//4.1e-111:804:81//U78090

F-NT2RP3003061//Human mRNA for ankyrin (variant 2.1).//1.4e-12:633:59//X16609

F-NT2RP3003068//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//0.034:282:60//AC002410

● F-NT2RP3003071//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse read cpg13d12.rt1c.//6.8e-15:95:100//Z64565

F-NT2RP3003078

F-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//8.1e-72:732:71//D88315

F-NT2RP3003121

F-NT2RP3003133//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.5e-12:168:76//AC004510

F-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//4.0e-148:908:87//D12646

F-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//2.0e-31:658:63//U17995

F-NT2RP3003145//Mus musculus carboxypeptidase X2 mRNA, complete cds.//3.

5e-22:430:63//AF017639

F-NT2RP3003150

F-NT2RP3003157//HS\_3055\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.9e-92:493:94//AQ155489

F-NT2RP3003185//Rattus norvegicus brain-enriched guanylate kinase-associated protein 1 mRNA, complete cds.//8.6e-06:228:65//AF064868

F-NT2RP3003193//H.sapiens HZF10 mRNA for zinc finger protein.//7.4e-73:7

37:71//X78933

F-NT2RP3003197

F-NT2RP3003203//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//4.1e-48:640:67//AF015264

F-NT2RP3003204//Human Mermaid LINE-1 element mRNA sequence.//0.0033:69:8  
1//U31059

F-NT2RP3003210//Homo sapiens SYBL1 gene.//1.1e-34:430:70//AJ004799

F-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1 C) mRNA, complete cds.//6.3e-75:776:74//U20286

F-NT2RP3003230//Rattus norvegicus mRNA for coronin-like protein.//1.8e-2:575:74//AJ006064

F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//3.7e-128:617:98//AF055460

F-NT2RP3003251//H.sapiens Staf50 mRNA.//3.5e-67:651:76//X82200

F-NT2RP3003264//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.015:473:58//AC 004153

F-NT2RP3003278//H.sapiens CpG island DNA genomic MseI fragment, clone 28 b4, forward read cpg28b4.ft1a.//4.0e-27:174:93//Z60555

F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//1.3e-131

:694:93//L36983

F-NT2RP3003290//*Homo sapiens* nickel-specific induction protein (Cap43) mRNA, complete cds.//1.7e-64:662:71//AF004162

F-NT2RP3003301//*Spinacia oleracea* mRNA for ATP-dependent protease Lon, complete cds.//4.9e-37:682:64//D85610

F-NT2RP3003302//*Homo sapiens*, clone hRPK.15\_A\_1, complete sequence.//4.6e-95:680:82//AC006213

F-NT2RP3003311//*Homo sapiens* chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//1.0:191:62//AC004527

F-NT2RP3003313//*Streptomyces coelicolor* cosmid 5A7.//0.0084:403:61//AL031107

F-NT2RP3003327//*H.sapiens* Staf50 mRNA.//2.5e-29:253:67//X82200

F-NT2RP3003330

F-NT2RP3003344

F-NT2RP3003346//*Homo sapiens* chromosome 17, clone hRPK.795\_F\_17, complete sequence.//9.0e-41:296:84//AC005284

F-NT2RP3003353//Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a BAC end-sequence (GSS).//0.047:404:60//AL021069

F-NT2RP3003377//*Homo sapiens* clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//8.3e-122:632:96//AC005519

F-NT2RP3003384//*Homo sapiens* Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unordered pieces.//0.0036:127:74//AC000360

F-NT2RP3003385//*Mus musculus* SKD3 mRNA, complete cds.//2.0e-110:843:79//U09874

F-NT2RP3003403//Human Chromosome X, complete sequence.//7.5e-21:647:61//AC002407

F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//1.0e-20:430:63//U90653

F-NT2RP3003411//*Mus musculus* COP9 complex subunit 7b (COPS7b) mRNA, comp

lete cds.//4.2e-139:524:90//AF071317

F-NT2RP3003427//HS-1051-A1-D03-MF.abi CIT Human Genomic Sperm Library C

Homo sapiens genomic clone Plate=CT 773 Col=5 Row=G, genomic survey sequence.//8.8e-18:111:97//B40173

F-NT2RP3003433//HS\_2219\_B2\_A11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=22 Row=B, genomic survey sequence.//1.2e-57:410:83//AQ145866

F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.2e-181:853:98//AF004828

● F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.6e-173:826:98//AB018268

F-NT2RP3003491//CIT-HSP-234401.TR CIT-HSP Homo sapiens genomic clone 234 401, genomic survey sequence.//1.2e-39:213:97//AQ057124

F-NT2RP3003500//HS\_3000\_B1\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.025:253:60//AQ090347

F-NT2RP3003543//Homo sapiens chromosome 16, cosmid clone 399H11 (LANL), complete sequence.//0.95:279:60//AC004234

● F-NT2RP3003552//Homo sapiens clone UWGC:y54c222 from 6p21, complete sequence.//1.8e-88:166:84//AC006049

F-NT2RP3003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//8.9e-17:245:72//AL031985

F-NT2RP3003564//HS\_3141\_B1\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3141 Col=19 Row=N, genomic survey sequence.//2.7e-79:442:93//AQ187798

F-NT2RP3003572

F-NT2RP3003576//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unsorted pieces.//5.8e-55:275:84//AC005632

F-NT2RP3003589//Canine rab10 mRNA for ras-related GTP-binding protein.//

1.1e-94:488:95//X56387

F-NT2RP3003621//*Homo sapiens* chromosome 16, cosmid clone 432A1 (LANL), complete sequence.//6.0e-88:463:84//AC004235

F-NT2RP3003625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 390E6, WORKING DRAFT SEQUENCE.//0.98:307:60//AL031600

F-NT2RP3003656

F-NT2RP3003659//*F.rubripes* GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271

F-NT2RP3003665//*Homo sapiens* chromosome 9q34, clone 63G10, complete sequence.//0.011:279:65//AC002096

F-NT2RP3003672

F-NT2RP3003680//*Drosophila melanogaster*; Chromosome 2R; Region 39B1-39B3; P1 clone DS05527, WORKING DRAFT SEQUENCE, 9 unordered pieces.//3.4e-16:425:64//AC005811

F-NT2RP3003686//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-27:153:98//AQ136993

F-NT2RP3003701

F-NT2RP3003716//*Rattus norvegicus* Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.6e-107:788:82//U42975

F-NT2RP3003726//*Homo sapiens* mRNA for KIAA0757 protein, complete cds.//3e-148:700:98//AB018300

F-NT2RP3003746//CIT-HSP-2306A10.TF CIT-HSP *Homo sapiens* genomic clone 2306A10, genomic survey sequence.//0.39:212:61//AQ015785

F-NT2RP3003795//Human DNA sequence from clone 333H23 on chromosome 22q12.1-12.3. Contains the (possibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold alternatively spliced gene for Synaptogyrin 1A, 1B and 1C (SYNGR1A, SYBGRIB, SYNGR1C), both genes downstream of a putative CpG island. Contains ESTs, an STS, GSSs, genomic mark

er D22S1155 and a ca repeat polymorphism, complete sequence.//4.2e-21:44  
5:66//AL022326

F-NT2RP3003799//Homo sapiens DNA from chromosome 19-cosmids R31158, R318  
74, and R28125, genomic sequence, complete sequence.//1.0:257:63//AF0384  
58

F-NT2RP3003800//Mouse neuronal proto-oncogene c-src mRNA encoding tyrosi  
ne-specific protein kinase, complete cds.//1.2e-63:484:81//M17031

F-NT2RP3003805//Homo sapiens chromosome 19, cosmid R27377, complete sequ  
ence.//0.96:353:60//AC005321

F-NT2RP3003809//Bovine herpesvirus 1 complete genome.//7.2e-12:615:60//A  
J004801

F-NT2RP3003819

F-NT2RP3003825

F-NT2RP3003828//Human rRNA primary transcript internal transcribed space  
r 2 (ITS2).//6.2e-16:543:62//X17626

F-NT2RP3003831//RPCI11-50N15.TJ RPCI11 Homo sapiens genomic clone R-50N1  
5, genomic survey sequence.//1.1e-21:174:85//AQ082633

F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//8.0e  
-47:242:98//AF070611

F-NT2RP3003842//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5,  
genomic survey sequence.//9.7e-25:143:97//AQ195884

F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds.//4.  
2e-36:335:68//AB018268

F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//4  
.1e-174:805:99//AB018343

F-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//2.7e-109:7  
09:84//U19181

F-NT2RP3003914//Drosophila melanogaster UDP-glucose:glycoprotein glucosy  
l transferase mRNA, complete cds.//8.9e-11:193:70//U20554

F-NT2RP3003918//*Homo sapiens* VAMP-associated protein of 33 kDa (VAP-33)

mRNA, complete cds.//2.6e-47:404:77//AF057358

F-NT2RP3003932//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1383 genomic

sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.68:597:55//AC

005504

F-NT2RP3003989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 404H4, WORKING DRAFT SEQUENCE.//0.37:548:56//AL031661

F-NT2RP3003992//Human cGMP-gated cation channel beta subunit (CNCG2) mRNA,  
complete cds.//0.021:433:58//U58837

● F-NT2RP3004013//*M. musculus* Spnr mRNA for RNA binding protein.//1.4e-164:  
838:94//X84692

F-NT2RP3004016//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 1018K9, WORKING DRAFT SEQUENCE.//0.00042:356:62//AL031726

F-NT2RP3004041//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 809F4, WORKING DRAFT SEQUENCE.//6.8e-112:627:82//AL022400

F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds.//2.2e-61:774  
:67//AB002317

● F-NT2RP3004070//*Homo sapiens* DNA sequence from PAC 352A20 on chromosome  
6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and  
slime mold hypothetical genes, and a gene coding for an aldehyde dehydr  
ogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.  
//7.9e-17:484:62//AL021939

F-NT2RP3004078//*M. musculus* (BALB/c) MRFX2 mRNA.//1.9e-102:684:83//X76089

F-NT2RP3004093//F24P17-Sp6 *Arabidopsis thaliana* genomic clone F24P17  
, genomic survey sequence.//0.021:207:63//B09433

F-NT2RP3004095//*Homo sapiens* clone NH0486I22, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//3.5e-25:272:77//AC005038

F-NT2RP3004110//*Homo sapiens* DNA from chromosome 19, BAC 33152, complete  
sequence.//8.6e-28:223:73//AC003973

F-NT2RP3004125//*Homo sapiens* TTF-I interacting peptide 20 mRNA, partial  
cds.//2.2e-28:637:63//AF000560

F-NT2RP3004145

F-NT2RP3004148

F-NT2RP3004155//*Homo sapiens* timing protein CLK-1 mRNA, complete cds.//6  
.5e-120:578:98//AF032900

F-NT2RP3004189//*M. musculus* tex292 mRNA (5' region).//1.1e-06:102:82//X804  
34

F-NT2RP3004206//*D. melanogaster* crn mRNA.//7.3e-69:715:71//X58374

F-NT2RP3004207//Mouse mRNA for seizure-related gene product 6 type 2 pre  
cursor, complete cds.//4.8e-42:650:66//D64009

F-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequen  
ce.//8.4e-55:184:84//D42052

F-NT2RP3004215//*Homo sapiens* chromosome 5, Pac clone 9c13 (LBNL H127), c  
omplete sequence.//0.22:458:60//AC006084

F-NT2RP3004242//*Caenorhabditis elegans* cosmid ZK632, complete sequence./  
/1.6e-29:409:69//Z22181

F-NT2RP3004246//*Homo sapiens* chromosome 10 clone CIT987SK-1010K1 map 10q  
25, complete sequence.//3.6e-117:242:100//AC005385

F-NT2RP3004253//*H. sapiens* 28S rRNA V8 region (LAN5-6).//2.6e-12:589:59//  
X69353

F-NT2RP3004258//*Rattus norvegicus* Zis mRNA, complete cds.//1.2e-88:489:9  
1//AF013967

F-NT2RP3004262//*Homo sapiens* heat shock protein hsp40-3 mRNA, complete c  
ds.//3.1e-153:733:98//AF088982

F-NT2RP3004282//*Homo sapiens* torsinA (DYT1) mRNA, complete cds.//1.3e-24  
:597:61//AF007871

F-NT2RP3004332

F-NT2RP3004334//*L. esculentum* gene for fruit ripening polygalacturonase./

/0.23:501:57//X80908

F-NT2RP3004341//Human DNA sequence from clone 503G16 on chromosome 6p23

Contains EST, CpG island, complete sequence.//0.0014:198:66//Z93020

F-NT2RP3004348//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.4e-103:600:82//X67877

F-NT2RP3004349//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-49:480:75//AC004025

F-NT2RP3004378//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23  
:352:67//AC005653

F-NT2RP3004399//H. sapiens mRNA for leucine-rich primary response protein 1.//7.2e-140:804:90//X97249

F-NT2RP3004424//Mus musculus mRNA for nuclear protein SA3.//6.8e-53:413:81//AJ005678

F-NT2RP3004428//Salmo salar DNA for a cryptic repeat.//3.2e-07:270:63//AJ012206

F-NT2RP3004451//RPCI11-51J15.TK RPCI11 Homo sapiens genomic clone R-51J15, genomic survey sequence.//8.8e-19:180:82//AQ052326

F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//6.2e-123:583:99//AB007917

F-NT2RP3004466//HS\_3038\_B2\_F08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=16 Row=L, genomic survey sequence.//0.41:172:59//AQ102458

F-NT2RP3004470//H. sapiens CpG island DNA genomic Mse1 fragment, clone 81a11, reverse read cpg81a11.rt1a.//7.0e-25:148:96//Z56029

F-NT2RP3004472//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//1.6e-20:143:92//AQ052792

F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-150:715:98//AB007925

F-NT2RP3004480//*Mus musculus* maternal-embryonic 3 (Mem3) mRNA, complete  
cds.//1.0e-119:679:90//U47024

F-NT2RP3004490//*Homo sapiens* mRNA for Musashi, complete cds.//7.1e-155:7  
52:97//AB012851

F-NT2RP3004498//*Homo sapiens* clone DJ1147A01, WORKING DRAFT SEQUENCE, 25  
unordered pieces.//4.0e-67:265:84//AC006023

F-NT2RP3004503//*Homo sapiens* Xp22-132-134 BAC GSHB-590J15 (Genome System  
s Human BAC library) complete sequence.//1.2e-55:415:78//AC004673

F-NT2RP3004504//*M. musculus* mRNA for CPEB protein.//2.0e-110:618:91//Y082  
60

F-NT2RP3004507//*Homo sapiens* chromosome 19, cosmid R26660, complete sequ  
ence.//9.3e-46:433:76//AC005328

F-NT2RP3004527//*Homo sapiens* mRNA; transcriptional unit N144, 5' end.//1  
.1e-100:508:97//AJ002574

F-NT2RP3004534//*Mouse oncogene (ect2)* mRNA, complete cds.//2.0e-93:442:8  
4//L11316

F-NT2RP3004539//*Homo sapiens* mRNA for KIAA0632 protein, partial cds.//8.  
5e-145:679:98//AB014532

F-NT2RP3004544//*Homo sapiens* mRNA for KIAA0554 protein, partial cds.//2.  
8e-169:793:98//AB011126

F-NT2RP3004566//*Mus musculus* krupple-related zinc finger protein (Emzf1)  
mRNA, complete cds.//6.9e-18:433:64//AF031955

F-NT2RP3004569//CITBI-E1-2522H6.TF CITBI-E1 *Homo sapiens* genomic clone 2  
522H6, genomic survey sequence.//5.3e-15:138:84//AQ280780

F-NT2RP3004572//*Homo sapiens* cofactor of initiator function (CIF150) mRN  
A, complete cds.//1.0e-179:860:97//AF026445

F-NT2RP3004578//*Homo sapiens* mRNA for KIAA0477 protein, complete cds.//4  
.2e-150:711:98//AB007946

F-NT2RP3004594//*Homo sapiens* mRNA for AND-1 protein.//1.1e-158:796:95//A

J006266

F-NT2RP3004617//*Homo sapiens* clone DJ1152C17, WORKING DRAFT SEQUENCE, 1  
unordered pieces.//9.3e-14:360:65//AC004977

F-NT2RP3004618//*Oryctolagus cuniculus* translation initiation factor eIF2  
C mRNA, complete cds.//2.9e-52:539:73//AF005355

F-NT2RP3004669//*Brn-3a*=class V POU transcription factor [mice, CD/CD, em  
bryo fibroblast cells, Genomic, 2160 nt].//0.046:437:57//S69350

F-NT2RP3004670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 356B8, WORKING DRAFT SEQUENCE.//1.9e-05:625:59//Z98882

● F-NT2RP4000008//*Homo sapiens* chromosome X, clone hCIT.200\_L\_4, complete  
sequence.//1.5e-155:844:92//AC006121

F-NT2RP4000023//*Arabidopsis thaliana* genomic DNA, chromosome 5, TAC clon  
e: K24G6, complete sequence.//0.012:417:59//AB012242

F-NT2RP4000035//*Homo sapiens* BAC clone NH0353P23 from 2, complete sequen  
ce.//8.0e-18:242:74//AC005035

F-NT2RP4000049//*Homo sapiens* decoy receptor 2 mRNA, complete cds.//2.1e-  
81:556:85//AF029761

● F-NT2RP4000051//*Mus musculus* mRNA for cartilage-associated protein (CASP  
).//1.6e-19:654:63//AJ006469

● F-NT2RP4000078//*Homo sapiens* mRNA for NS1-binding protein (NS1-BP).//2.5  
e-149:720:97//AJ012449

F-NT2RP4000102//*Plasmodium falciparum* MAL3P2, complete sequence.//0.28:3  
36:57//AL034558

F-NT2RP4000109//*Homo sapiens* mRNA for MEGF5, partial cds.//4.4e-166:774:  
99//AB011538

F-NT2RP4000111//*B. taurus* mRNA for cleavage and polyadenylation specifici  
ty factor.//2.6e-137:678:91//X75931

F-NT2RP4000129//*Homo sapiens* mRNA for KIAA0483 protein, partial cds.//3.  
3e-114:548:98//AB007952

F-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.2e-104:677:85//U35776

F-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//7.2e-54:327:74//L20681

F-NT2RP4000151//Homo sapiens clone 664 unknown mRNA, partial sequence.//2.2e-62:360:92//AF091088

F-NT2RP4000159//RPCI11-75N16.TJ RPCI11 Homo sapiens genomic clone R-75N16, genomic survey sequence.//2.6e-19:119:98//AQ267551

F-NT2RP4000167//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//3.3e-49:683:67//AC006210

F-NT2RP4000185//Homo sapiens clone DT1P1E11 mRNA, CAG repeat region.//1.1e-99:543:93//U92989

F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.9e-174:825:98//AB014600

F-NT2RP4000212//, complete sequence.//4.0e-131:233:94//AC005300

F-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.8e-161:751:99//AC005261

F-NT2RP4000218//RPCI11-69B7.TJ RPCI11 Homo sapiens genomic clone R-69B7, genomic survey sequence.//1.7e-84:413:98//AQ268504

F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//2.6e-156:771:97//AJ006470

F-NT2RP4000246//Mus musculus neural variant mena+++ protein (Mena) mRNA, complete cds.//2.1e-120:707:87//U72523

F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//2.8e-128:604:99//AF091092

F-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.27:124:69//AQ043515

F-NT2RP4000290//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-32:619:63//Z71408

F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds.//4.7e-41:685:

63//D63481

F-NT2RP4000321//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//6.9e-05:756:59//U59322

F-NT2RP4000323

F-NT2RP4000355

F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.0e-140:654:99//AB018281

F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//2.6e-135:649:97//AF044195

F-NT2RP4000370//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//2.0e-23:524:62//AJ235272

F-NT2RP4000376//Sequence 1 from patent US 5580968.//1.6e-115:716:87//I30536

F-NT2RP4000381//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//4.3e-05:450:58//D63850

F-NT2RP4000398//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//9.2e-37:336:69//AC006116

F-NT2RP4000415//Caenorhabditis elegans cosmid C42D8.//0.30:222:60//U56966

F-NT2RP4000417//Drosophila melanogaster cosmid clone 86E4.//1.8e-48:580:69//AL021086

F-NT2RP4000424//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.6e-42:265:81//AC003101

F-NT2RP4000448//CIT-HSP-2370F8.TF CIT-HSP Homo sapiens genomic clone 230F8, genomic survey sequence.//2.0e-56:287:98//AQ110194

F-NT2RP4000449//CIT-HSP-2366N18.TR CIT-HSP Homo sapiens genomic clone 2366N18, genomic survey sequence.//2.4e-42:236:95//AQ076183

F-NT2RP4000455//Homo sapiens PAC clone 166H1 from 12q, complete sequence

./.0.17:158:67//AC003982

F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP).//0.00034:532:57//Z72499

F-NT2RP4000480//Rhodothermus marinus R-21 DNA ligase gene, complete cds.  
//0.0094:616:58//U10483

F-NT2RP4000481

F-NT2RP4000498//S.cerevisiae chromosome IX cosmid 9150.//5.7e-24:633:60/  
/Z38125

F-NT2RP4000500//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//2  
.4e-62:667:73//X74904

F-NT2RP4000515

F-NT2RP4000517//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//1.6e-179:851:98//AC006238

F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//6.7e-33:203:93//AJ010840

F-NT2RP4000519//Mus musculus tyrosine kinase growth factor receptor (Etk 2/tyro3) gene, alternative 5' coding exon 2C.//0.26:162:61//U23720

F-NT2RP4000524//Rattus norvegicus rsec8 mRNA, partial cds.//1.2e-139:809  
:89//U32498

F-NT2RP4000528//Caenorhabditis elegans cosmid F59E12.//1.0e-06:404:59//AF003386

F-NT2RP4000541//Drosophila melanogaster DNA sequence (P1 DS02109 (D53)), complete sequence.//1.3e-05:498:58//AC002443

F-NT2RP4000556//Sequence 1 from Patent EP 0285405.//1.2e-18:586:61//I054  
65

F-NT2RP4000560//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//2.5e-53:183:82//AF059580

F-NT2RP4000588//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 414D7, WORKING DRAFT SEQUENCE.//0.00062:253:65//AL033543

F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//3.2e-138:666:98//AF067730

F-NT2RP4000638//HS\_3042\_B2\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence.//3.0e-06:78:89//AQ099333

F-NT2RP4000648//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds.//1.9e-11:104:85//AB017335

● F-NT2RP4000657//Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1.//0.34:350:62//AF100904

F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856.//3.3e-167:785:99//AB004852

F-NT2RP4000713//Gallus gallus atonal homolog 1 (Cath1) gene, complete cds.//3.7e-07:261:65//U61149

F-NT2RP4000724//Human endogenous retrovirus env mRNA.//9.2e-136:474:89//X82272

F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds.//3.1e-41:350:71//AB011178

● F-NT2RP4000737//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds.//1.0:504:58//L19301

F-NT2RP4000739//CIT-HSP-2010022.TR CIT-HSP Homo sapiens genomic clone 20 10022, genomic survey sequence.//1.1e-24:161:93//B57903

F-NT2RP4000781//Homo sapiens clone DJ0892G19, complete sequence.//0.052:493:58//AC004917

F-NT2RP4000787//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//9.6e-18:259:68//U2281

F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//1

.5e-174:816:98//AB007939

F-NT2RP4000833//*Homo sapiens* PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.97:52:92//AC005189

F-NT2RP4000837//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE.//2.1e-128:644:97//AL034420

F-NT2RP4000839//RPCI11-6D8.TP RPCI-11 *Homo sapiens* genomic clone RPCI-11-6D8, genomic survey sequence.//1.5e-44:281:91//B48216

F-NT2RP4000855//*Rattus norvegicus* mRNA for aminopeptidase-B, complete cds.//9.5e-43:722:64//D87515

F-NT2RP4000865//Human zinc finger protein ZNF136.//6.8e-95:415:78//U0936  
7

F-NT2RP4000878//*Mus musculus* mRNA for myeloid associated differentiation protein.//7.0e-87:646:80//AJ001616

F-NT2RP4000879//*N.tabaccum* mRNA for ubiquitin activating enzyme E1.//9.0e-17:806:58//Y10804

F-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.//6.8e-153:934:86//D45913

F-NT2RP4000915//*Homo sapiens* mRNA for ZNF198 protein.//9.4e-79:584:78//AJ224901

F-NT2RP4000918//*Drosophila melanogaster* DNA sequence (P1 DS04106 (D172)), complete sequence.//2.0e-08:609:58//AC004290

F-NT2RP4000925//*Rattus norvegicus* Shal-related potassium channel Kv4.3 mRNA, complete cds.//3.5e-64:415:87//U42975

F-NT2RP4000927//*H.sapiens* genomic DNA (chromosome 3; clone NRL062R).//0.75:175:62//X87547

F-NT2RP4000928//*Homo sapiens* CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//3.5e-163:781:97//AF069532

F-NT2RP4000929//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.94:763:56//AC00

4688

F-NT2RP4000955//*Homo sapiens* clone DJ0919J22, WORKING DRAFT SEQUENCE, 34  
unordered pieces.//1.0e-128:673:96//AC005519

F-NT2RP4000973//*Caenorhabditis elegans* cosmid Y47H9C, complete sequence.  
//1.6e-15:255:69//AL032657

F-NT2RP4000975//CIT-HSP-2307I6.TF CIT-HSP *Homo sapiens* genomic clone 230  
7I6, genomic survey sequence.//6.5e-31:317:79//AQ015742

F-NT2RP4000979//Human bullous pemphigoid antigen mRNA, 3' end.//0.88:54:  
90//M22942

● F-NT2RP4000984//*Rhodobacter sphaeroides* mRNA.//0.76:214:64//M83823

F-NT2RP4000989//*F. rubripes* GSS sequence, clone 011A11aE12, genomic survey  
sequence.//1.0:149:65//AL010911

F-NT2RP4000996//*Penaeus setiferus* microsatellite Pse017 repeat region.//  
3.3e-08:139:74//AF047358

F-NT2RP4000997//*Rattus norvegicus* RNA polymerase I 127 kDa subunit mRNA,  
complete cds.//3.6e-126:824:84//AF025424

F-NT2RP4001004

● F-NT2RP4001006//*Mus musculus* ROSA 26 transcription AS ROSA26AS mRNA, complete  
cds.//1.4e-110:861:78//U83176

● F-NT2RP4001010//*Rattus norvegicus* PSD-95/SAP90-associated protein-4 mRNA  
, complete cds.//2.0e-135:789:89//U67140

F-NT2RP4001029//*Mus domesticus* nuclear binding factor NF2d9 mRNA, complete  
cds.//3.7e-120:718:88//U20086

F-NT2RP4001041//*Schizosaccharomyces pombe* mRNA, partial cds, clone: SY 0  
717.//4.1e-22:452:64//D89170

F-NT2RP4001057

F-NT2RP4001064//*Mus musculus* mRNA for cartilage-associated protein (CASP)  
).//1.2e-20:639:62//AJ006469

F-NT2RP4001078//*Streptomyces coelicolor* cosmid 1C2.//0.0025:474:59//AL03

1124

F-NT2RP4001079//Rat alternatively spliced mRNA.//1.4e-141:832:88//M93018

F-NT2RP4001080//H.sapiens PTB-4 gene for polypyrimidine tract binding protein.//9.0e-64:628:70//X65372

F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds.//4.7e-84:604:86//AB011164

F-NT2RP4001095

F-NT2RP4001100//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2 503J7, genomic survey sequence.//9.4e-17:185:79//AQ263402

F-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//1.0e-143:760:87//M96629

F-NT2RP4001122

F-NT2RP4001126//Homo sapiens shox gene, alternatively spliced products, complete cds.//4.2e-17:636:61//U82668

F-NT2RP4001138//Homo sapiens PAC clone DJ1121E10 from 7q21.1-q2, complete sequence.//2.5e-23:408:60//AC004969

F-NT2RP4001143//Sequence 5 from patent US 5753432.//1.8e-39:276:86//AR00 8079

F-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unorderd pieces.//2.7e-116:684:89//AC005095

F-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//3.0e-48:581:66//D67067

F-NT2RP4001150//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unorderd pieces.//9.4e-25:193:67//AC004952

F-NT2RP4001159//Human FMR1 gene, 5' end.//0.28:130:66//L19476

F-NT2RP4001174//FMR1 {CGG repeats} [human, Fragile X syndrome patient, genomic, 429 nt].//0.0014:187:67//S74494

F-NT2RP4001206//Dictyostelium discoideum random slug cDNA19 protein (rsc 19) mRNA, partial cds.//0.032:453:58//U82511

F-NT2RP4001207//HS\_2248\_A1\_C03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=5 Row=E, genomic survey sequence.//0.00018:58:94//AQ192358

F-NT2RP4001210//Homo sapiens chromosome 10 clone CIT987SK-1019018 map 10 p11.2-10p12.1, complete sequence.//0.93:515:58//AC005877

F-NT2RP4001213//Human KRAB zinc finger protein (ZNF177) mRNA, splicing variant, complete cds.//3.6e-44:187:74//U37251

F-NT2RP4001219//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.3e-15:288:67//AL032657

F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.2e-26:855:60//AF059569

F-NT2RP4001235//RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-18E11, genomic survey sequence.//2.7e-15:101:98//B88081

F-NT2RP4001256//Amycolatopsis mediterranei 3-amino-5-hydroxy benzoic acid synthase (rifD) gene, complete cds.//1.0:459:59//U33061

F-NT2RP4001260//Sequence 2 from Patent WO9601901.//0.0018:246:63//A48324

F-NT2RP4001274//Homo sapiens, complete sequence.//2.5e-05:201:67//AC005854

F-NT2RP4001276//CIT-HSP-2324B15.TF CIT-HSP Homo sapiens genomic clone 2324B15, genomic survey sequence.//3.5e-18:138:92//AQ040728

F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//7.4e-30:535:65//AF043250

F-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//3.5e-145:795:91//AJ001119

F-NT2RP4001336//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109:94//B89870

F-NT2RP4001339//HS\_3205\_B1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=15 Row=J, genomic survey

sequence.//7.1e-24:305:73//AQ183725

F-NT2RP4001343//Homo sapiens PAC clone DJ0894A10 from 7q32-q32, complete sequence.//1.9e-17:106:91//AC004918

F-NT2RP4001345//G.gallus mRNA for lecithin-cholesterol acyltransferase.//7.6e-40:631:66//X91011

F-NT2RP4001351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 184J9, WORKING DRAFT SEQUENCE.//2.7e-30:608:64//AL031428

F-NT2RP4001353//Streptomyces coelicolor cosmid 5A7.//0.23:540:57//AL031107

F-NT2RP4001372//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//8.5e-23:129:100//AQ051701

F-NT2RP4001373//G.gallus genomic DNA repeat region, clone 16E1.//0.15:213:61//X78609

F-NT2RP4001375

F-NT2RP4001379//Homo sapiens chromosome 17, clone hRPK.311\_F\_12, complete sequence.//7.3e-28:153:88//AC005722

F-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//7.2e-47:518:73//AC004691

F-NT2RP4001407//P.falciparum glutamic acid-rich protein gnen, complete cds.//0.00079:686:57//J03998

F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds.//2.0e-76:818:71//D86957

F-NT2RP4001433//H.sapiens HZF10 mRNA for zinc finger protein.//3.5e-87:839:73//X78933

F-NT2RP4001442

F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds.//0.21:218:63//AB018326

F-NT2RP4001474//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884

F-NT2RP4001483//Human mRNA for 2-oxoglutarate dehydrogenase, complete cds.//2.5e-59:480:75//D10523

F-NT2RP4001498//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//9.7e-39:392:72//AF049612

F-NT2RP4001502//H.sapiens (D8S135) DNA segment containing GT repeat.//2.7e-24:147:96//X61693

F-NT2RP4001507//Plasmid pSB24.2 (from S.cyanogenus) neomycin resistance protein gene, complete cds.//0.87:583:58//M32513

F-NT2RP4001524//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.93:394:58//AC05308

F-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.1e-143:820:89//U20086

F-NT2RP4001547//S.cerevisiae chromosome XIV reading frame ORF YNR048w.//2.2e-05:319:61//Z71663

F-NT2RP4001551//S.pombe chromosome II p1 p8B7.//0.64:335:60//AL032684

F-NT2RP4001555//Homo sapiens 12q24.2 BAC RPCI11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.0:309:58//AC004806

F-NT2RP4001567//HS\_2166\_B1\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=13 Row=F, genomic survey sequence.//0.99:188:59//AQ086290

F-NT2RP4001568//Human mRNA for KIAA0167 gene, complete cds.//7.0e-53:566:72//D79989

F-NT2RP4001571//RPCI11-21F20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F20, genomic survey sequence.//2.8e-19:119:97//B85885

F-NT2RP4001574//B.primigenius mRNA for coat protein gamma-cop.//5.8e-129:813:85//X92987

F-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//3.4e-131:795:8

6//AJ223830

F-NT2RP4001592//*S.aureus* gene for isoleucyl-tRNA synthetase.//1.3e-14:66  
3:59//X74219

F-NT2RP4001610//*Homo sapiens* Xp22 Cosmids U15E4, U115H5, U132E12, U115B9  
(Lawrence Livermore human cosmid library) complete sequence.//6.4e-10:  
135:73//AC002364

F-NT2RP4001614//HS\_3042\_B2\_D05\_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence.//3.4e-06:78:89//AQ099333

F-NT2RP4001634

F-NT2RP4001638//cSRL-161F1-u cSRL flow sorted Chromosome 11 specific cosmid *Homo sapiens* genomic clone cSRL-161F1, genomic survey sequence.//4.9e-12:144:76//B02870

F-NT2RP4001644//*M.musculus* mRNA for map kinase interacting kinase, Mnk2.  
//3.8e-69:437:86//Y11092

F-NT2RP4001656//HS\_2013\_A1\_D01\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2013 Col=1 Row=G, genomic survey sequence.//2.0e-30:207:89//AQ224793

F-NT2RP4001677//*Hylobates lar* huntingtin gene, partial exon.//0.23:105:7  
1//L49362

F-NT2RP4001679//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462023, WORKING DRAFT SEQUENCE.//2.7e-45:351:84//AL031431

F-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.8e-30:163:88//U96629

F-NT2RP4001725//*Drosophila melanogaster* DNA sequence (P1 DS08860 (D181)), complete sequence.//1.1e-13:402:63//AC004296

F-NT2RP4001730//RPCI11-37M21.TK RPCI-11 *Homo sapiens* genomic clone RPCI-11-37M21, genomic survey sequence.//0.88:177:67//AQ029840

F-NT2RP4001739

F-NT2RP4001753//H.sapiens telomeric DNA sequence, clone 12QTEL023, read  
12QTEL00023.seq.//4.9e-36:192:98//Z96232

F-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//2.3e-140:866:  
86//L11316

F-NT2RP4001790//Homo sapiens clone NH0569I24, complete sequence.//1.4e-2  
9:327:74//AC005678

F-NT2RP4001803

F-NT2RP4001822//Homo sapiens tetraspan TM4SF (TSPAN-4) mRNA, complete cd  
s.//1.0e-16:576:60//AF054841

● F-NT2RP4001823//Human DNA sequence from clone 181C9 on chromosome 22q13.  
2-13.33. Contains a PHAPI2 Leucine Rich Acidic Nuclear Protein pseudogen  
e, part of a putative novel gene, ESTs, STSs and GSSs, complete sequence  
.//2.1e-08:601:59//Z98743

F-NT2RP4001828

F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds.//2.2e-53:555:  
73//D31888

F-NT2RP4001841

F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds.//1  
.7e-55:813:65//AB014572

● F-NT2RP4001861//Human simple repeat polymorphism.//0.0014:145:66//M87691

F-NT2RP4001889//HS\_2052\_B1\_H06\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2052 Col=11 Row=P, genomic survey  
sequence.//1.0e-23:187:86//AQ270425

F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequ  
ence.//7.3e-76:178:95//AC005014

F-NT2RP4001896//T3B4TFC TAMU *Arabidopsis thaliana* genomic clone T3B4, ge  
nomic survey sequence.//0.99:354:61//B26193

F-NT2RP4001901//*Streptomyces griseus* genes for Orf2, Orf3, Orf4, Orf5, A  
fsA, Orf8, partial and complete cds.//0.031:409:60//AB011413

F-NT2RP4001927//HS\_2216\_B1\_D03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=5 Row=H, genomic survey sequence.//4.9e-32:216:89//AQ184677

F-NT2RP4001938//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.2e-83:709:79//U49046

F-NT2RP4001946//HS\_3021\_B2\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=20 Row=P, genomic survey sequence.//7.6e-09:120:76//AQ133185

F-NT2RP4001950//Human DNA sequence from clone 353H6 on chromosome Xq25-2

● 6.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSSs and GSSs, complete sequence.//2.1e-18:421:65//AL022577

F-NT2RP4001953//CIT-HSP-2294D14.TR CIT-HSP Homo sapiens genomic clone 22 94D14, genomic survey sequence.//0.030:358:61//AQ005028

F-NT2RP4001966//Mus musculus DOC4 (Doc4) mRNA, complete cds.//2.5e-68:81 2:68//AF059485

F-NT2RP4001975//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence.//1.9e-57:555:75//AC003976

● F-NT2RP4002018//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence.//8.9 e-21:123:98//B01950

F-NT2RP4002047//Saccharomyces cerevisiae chromosome XII cosmid 8003.//1. 6e-29:520:64//U17243

F-NT2RP4002052//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 20 45A15, genomic survey sequence.//2.8e-22:137:96//B80243

F-NT2RP4002058//T20L11-T7 TAMU Arabidopsis thaliana genomic clone T20L11, genomic survey sequence.//0.019:141:65//AQ248640

F-NT2RP4002071//CIT-HSP-2314J9.TF CIT-HSP Homo sapiens genomic clone 231

4J9, genomic survey sequence.//0.99:163:63//AQ027223

F-NT2RP4002075//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*

\* from clone Y57G11, WORKING DRAFT SEQUENCE.//0.15:506:59//Z92841

F-NT2RP4002078//RPCI11-73M20.TJ RPCI11 *Homo sapiens* genomic clone R-73M20, genomic survey sequence.//4.8e-21:130:96//AQ269030

F-NT2RP4002081//*F. rubripes* GSS sequence, clone 190022bB9, genomic survey sequence.//0.0024:350:60//Z92062

F-NT2RP4002083//*M. musculus* tex27 mRNA.//8.2e-77:456:89//X80437

F-NT2RP4002408//*Caenorhabditis elegans* serine/threonine kinase LET-502 (let-502) mRNA, complete cds.//3.7e-18:541:62//U85515

F-NT2RP4002791

F-NT2RP4002888//*Homo sapiens* BAC clone RG067E13 from 7q21, complete sequence.//4.7e-39:385:75//AC002383

F-NT2RP4002905//*Homo sapiens* chromosome 17, clone hRPC.842\_A\_23, complete sequence.//6.5e-91:672:83//AC004662

F-NT2RP5003459//Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds.//2.9e-37:193:99//M33197

F-NT2RP5003461//Human DNA sequence from PAC 506G2 contains ESTs.//7.9e-5 1:300:80//Z82901

F-NT2RP5003477//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.7e-77:150:100//AC000380

F-NT2RP5003492

F-NT2RP5003500//Human DNA sequence from cosmid 97K10, between markers DX S6791 and DDX8038 on chromosome X contains STSs and CpG island.//1.7e-11 1:623:93//Z81365

F-NT2RP5003506//*H. sapiens* CpG island DNA genomic Mse1 fragment, clone 71 h2, reverse read cpg71h2.rt1a.//1.4e-49:283:93//Z62703

F-NT2RP5003512//HS\_3084\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3084 Col=7 Row=G, genomic survey s

equence.//7.7e-18:117:95//AQ186312

F-NT2RP5003522//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12  
unordered pieces.//3.8e-101:211:96//AC005236

F-NT2RP5003524//Homo sapiens beta-spectrin (HSPTB1) gene, exon 14 and pa  
rtial cds.//0.00056:650:57//AF013178

F-NT2RP5003534//H.sapiens CpG island DNA genomic Mse1 fragment, clone 14  
c10, forward read cpg14c10.ft1b.//0.00013:70:91//Z54631

F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.  
2e-67:373:94//AB007934

● F-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complet  
e sequence.//5.8e-93:518:81//AC005510

F-OVARC1000006//Gallus gallus histone H2A (H2A-VIII) gene, complete cds.  
//9.1e-56:392:84//U38933

F-OVARC1000013

F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//5.6e-170:8  
15:98//AF058922

F-OVARC1000017//Streptomyces glaucescens tcm operon.//0.37:347:60//M8067  
4

● F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds.//6.8e-36:2  
38:89//AF064603

F-OVARC1000058

F-OVARC1000060//Homo sapiens ribonuclease 6 precursor, mRNA, complete cd  
s.//2.5e-36:192:98//U85625

F-OVARC1000068//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 404K8, WORKING DRAFT SEQUENCE.//0.14:554:57//AL023883

F-OVARC1000071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 596C15, WORKING DRAFT SEQUENCE.//5.3e-104:197:100//AL031387

F-OVARC1000085//Human DNA sequence from clone 191N21 on chromosome 6q27  
Contains genes for PDCD2 (PROGRAMMED CELL DEATH-2/RP8 HOMOLOG), TATA fac

tor (TFIID), proteasome subunit HC5, EST, STS, GSS, complete sequence.//  
1.6e-116:588:96//AL031259

F-OVARC1000087//HS\_2004\_B2\_E11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2004 Col=22 Row=J, genomic survey sequence.//7.1e-11:94:94//AQ221037

F-OVARC1000091//nbxb0020P17r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020P17r, genomic survey sequence.//5.2e-05:238:64//AQ258489

F-OVARC1000092//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.1e-10:720:58//AC004617

● F-OVARC1000106//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//9.9e-05:141:73//AQ175369

F-OVARC1000109

F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.6e-133:663:96//AF069250

F-OVARC1000114//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING DRAFT SEQUENCE.//2.3e-51:547:70//AL022574

F-OVARC1000133//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.62:349:61//AC005027

● F-OVARC1000139//Caenorhabditis elegans cosmid F09D1.//2.5e-18:314:64//AF040640

F-OVARC1000145//HS\_2257\_B2\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=22 Row=H, genomic survey sequence.//5.8e-30:203:90//AQ304854

F-OVARC1000148//CIT-HSP-2345A22.TR CIT-HSP Homo sapiens genomic clone 2345A22, genomic survey sequence.//1.1e-26:146:100//AQ056703

F-OVARC1000151//Sequence 1 from patent US 5665588.//2.6e-61:677:70//I646  
95

F-OVARC1000168//Homo sapiens chromosome 19, cosmid R31343, complete sequ

ence.//4.9e-19:381:63//AC005764

F-OVARC1000191//**Plasmodium falciparum** DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from MAL4P1, WORKING DRAFT SEQUENCE.//1.3e-06:745:57//AL034557

F-OVARC1000198//\*\*\* SEQUENCING IN PROGRESS \*\*\* **Homo sapiens** chromosome 4  
, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered  
pieces.//6.4e-161:781:97//AC004604

F-OVARC1000209//**Oryza sativa** submergence induced protein 2A mRNA, comple  
te cds.//9.2e-33:511:65//AF068332

F-OVARC1000212//**F.rubripes** GSS sequence, clone 185L11aC1, genomic survey  
sequence.//1.1e-13:139:79//AL019910

F-OVARC1000240//Sequence 1 from patent US 5710024.//1.4e-129:623:98//I181  
226

F-OVARC1000241//**Mus musculus** hypoxia inducible factor three alpha mRNA,  
complete cds.//1.1e-112:697:87//AF060194

F-OVARC1000288

2.2e-22:181:83//J00345

F-OVARC1000302//A-192A9.TP CIT978SK **Homo sapiens** genomic clone A-192A9,  
genomic survey sequence.//4.8e-18:110:99//B18003

F-OVARC1000304//Mouse mRNA from Mov10 locus.//5.5e-100:631:85//X52574

F-OVARC1000309

F-OVARC1000321//**Homo sapiens** clone NH0479C13, WORKING DRAFT SEQUENCE, 12  
unordered pieces.//3.1e-122:325:95//AC005236

F-OVARC1000326//**Rattus norvegicus** lamina-associated polypeptide 1C (LAP1  
C) mRNA, complete cds.//4.0e-46:339:84//U19614

F-OVARC1000335//**Caenorhabditis elegans** cosmid F15B10.//0.020:545:57//AF  
36696

F-OVARC1000347//**Homo sapiens** clone GS051M12, complete sequence.//0.71:25  
2:59//AC005007

F-OVARC1000384//**Homo sapiens** expanded SCA7 CAG repeat.//2.2e-09:276:64//

AF020275

F-OVARC1000408//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing K  
vLQT1 gene, complete sequence.//0.61:343:59//AC003693

F-OVARC1000411//S.cerevisiae chromosome XI reading frame ORF YKL202w.//0  
.075:242:60//Z28201

F-OVARC1000414//Homo sapiens PAC clone DJ0905M06 from 7q31, complete seq  
uence.//0.00088:285:62//AC005166

F-OVARC1000420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 371H6, WORKING DRAFT SEQUENCE.//0.14:487:60//AL031718

● F-OVARC1000427//Homo sapiens clone UWGC:rg041a03 from 7p14-15, complete  
sequence.//4.9e-30:195:84//AC005826

F-OVARC1000431//Plasmodium falciparum MAL3P2, complete sequence.//1.3e-0  
5:651:59//AL034558

F-OVARC1000437//Chicken tensin mRNA, complete cds.//9.6e-54:296:78//M741  
65

F-OVARC1000440//Human PINCH protein mRNA, complete cds.//2.7e-19:116:99/  
/U09284

● F-OVARC1000442//Human DNA sequence from clone 816K17 on chromosome 20p12  
.2-13 Contains TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR  
(EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3), and another member of the  
Transglutaminase family, complete sequence.//1.0e-21:202:79//AL031678

F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1  
.0e-138:566:99//AB014583

F-OVARC1000461

F-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1  
) mRNA, complete cds.//4.7e-124:650:93//AF023451

F-OVARC1000466//Homo sapiens DNA from chromosome 19, cosmid R29144, comp  
lete sequence.//1.0e-15:510:59//AC004221

F-OVARC1000473//Ciona intestinalis genomic fragment, clone 3F4, genomic

survey sequence.//2.5e-06:272:62//AJ227191

F-OVARC1000479//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.1e-117:652:90//E12829

F-OVARC1000486//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//1.7e-13:709:60//Z99297

F-OVARC1000496//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//6.0e-23:316:72//AL031733

F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.1e-113:539:99//AF051850

F-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces.//8.0e-149:716:98//AC005024

F-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//5.8e-137:545:97//AC004510

F-OVARC1000543//HS\_3055\_A2\_F10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=20 Row=K, genomic survey sequence.//0.19:104:71//AQ102820

F-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS, CpG island, complete sequence.//4.4e-136:670:97//AL022069

F-OVARC1000557//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence.//1.3e-15:262:69//AC002985

F-OVARC1000564//Mus musculus clone OST7314, genomic survey sequence.//1.9e-41:476:70//AF046733

F-OVARC1000573//HS\_3241\_B1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=5 Row=P, genomic survey sequence.//2.2e-101:530:95//AQ211942

F-OVARC1000576//Human Chromosome X, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.7e-97:445:90//AC002414

F-OVARC1000578//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//9.1e-27:354:72//AC003973

F-OVARC1000588//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence.//0.97:276:62//AL023775

F-OVARC1000605

F-OVARC1000622//Homo sapiens (subclone 2\_d8 from P1 H42) DNA sequence, complete sequence.//7.2e-60:457:82//L81648

F-OVARC1000640//Human BAC clone RG326K09 from 7q21, complete sequence.//6.2e-58:499:80//AC002069

F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//5.1e-77:424:93//D43772

F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//4.8e-99:536:94//AB011162

F-OVARC1000678//cSRL-29c7-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-29c7, genomic survey sequence.//2.5e-57:336:91//B04244

F-OVARC1000679//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.6e-81:291:84//AJ001713

F-OVARC1000681//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING DRAFT SEQUENCE.//8.2e-158:782:96//AL034424

F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.5e-151:549:99//AF027156

F-OVARC1000689//nbxb0003aG01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003M01f, genomic survey sequence.//0.17:499:60//AQ050003

F-OVARC1000700

F-OVARC1000703//*Drosophila melanogaster* DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//3.5e-26:425:65//U34925

F-OVARC1000722//*Homo sapiens* chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.//3.7e-109:451:91//AF038661

F-OVARC1000730

F-OVARC1000746

F-OVARC1000769//HS\_2056\_B2\_G06\_T7 CIT Approved Human Genomic Sperm Library D. *Homo sapiens* genomic clone Plate=2056 Col=12 Row=N, genomic survey sequence.//8.8e-19:147:86//AQ245905

● F-OVARC1000771//*M. musculus* mRNA for GTP-binding protein.//2.2e-62:305:78//X95403

F-OVARC1000781//Sequence 5 from Patent W09722695.//1.9e-89:705:78//A6355  
2

F-OVARC1000787//*Homo sapiens* PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.0e-131:631:98//AC004542

F-OVARC1000800//Human Chromosome 11q23 PAC clone pDJ254e13, complete sequence.//1.7e-32:295:80//AC003691

● F-OVARC1000802//*Homo sapiens* chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//3.2e-55:356:88//AC004469

● F-OVARC1000834//*Homo sapiens* mRNA for atopy related autoantigen CALC.//9.5e-27:163:94//Y17711

F-OVARC1000846//*Homo sapiens* mRNA for KIAA0643 protein, partial cds.//6.0e-150:432:100//AB014543

F-OVARC1000850//*Homo sapiens* PB39 mRNA, complete cds.//1.0e-135:632:99//AF045584

F-OVARC1000862//*M. musculus* mRNA for FT1.//2.6e-109:769:83//Z67963

F-OVARC1000876//*S.cerevisiae* chromosome IX cosmid 9150.//7.4e-21:541:61//Z38125

F-OVARC1000883//*Mus domesticus* nuclear binding factor NF2d9 mRNA, comple

te cds.//2.2e-08:98:88//U20086

F-OVARC1000885//B.subtilis 25 kb genomic DNA segment (from sspE to kata)

//0.25:231:61//Z82044

F-OVARC1000886//CIT-HSP-2171H6.TR CIT-HSP Homo sapiens genomic clone 217  
1H6, genomic survey sequence.//0.00035:139:69//B89721

F-OVARC1000890

F-OVARC1000891

F-OVARC1000897//Human DNA sequence from clone 215F16 on chromosome 22q12  
.1-12.3. Contains part of a Homeobox domain containing gene and GSSs, co  
mplete sequence.//1.4e-18:473:64//AL024494

F-OVARC1000912//Bovine herpesvirus type 1 early-intermediate transcripti  
on control protein (BICP4) gene, complete cds.//8.9e-08:378:63//L14320

F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds.//7.  
7e-85:440:95//AB011172

F-OVARC1000924//HS\_2022\_A1\_C01\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2022 Col=1 Row=E, genomic survey s  
equence.//5.7e-21:122:99//AQ269493

F-OVARC1000936//Human PAC clone DJ0093I03 from Xq23, complete sequence.//  
1.2e-113:476:91//AC003983

F-OVARC1000937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 20208, WORKING DRAFT SEQUENCE.//0.00066:436:61//AL031848

F-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding  
protein, complete cds.//5.0e-89:556:86//AB005549

F-OVARC1000948//P.falciparum complete gene map of plastid-like DNA (IR-B  
).//0.98:160:64//X95276

F-OVARC1000959//CIT-HSP-2348016.TR CIT-HSP Homo sapiens genomic clone 23  
48016, genomic survey sequence.//0.99:270:59//AQ062850

F-OVARC1000960//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1  
p35. Contains delta opiate receptor, CpG island, CA repeat.,//3.9e-41:57

7:72//AL009181

F-OVARC1000964//*P.falciparum* malaria antigen (M26-32-2) gene, partial cds.//0.19:83:73//M63270

F-OVARC1000971//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y57G11, WORKING DRAFT SEQUENCE.//0.013:670:57//Z92841

F-OVARC1000984//*Leishmania major* chromosome 1, complete sequence.//0.80:  
345:58//AE001274

F-OVARC1000996//M025 gene [mice, embryos, mRNA, 2322 nt].//2.6e-55:403:8  
2//S51858

F-OVARC1000999//Synthetic construct galanin receptor type 3 (GALR3) gene  
, complete cds.//0.33:105:69//AF042785

F-OVARC1001000//HS\_2247\_A1\_H05\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2247 Col=9 Row=0, genomic survey sequence.//3.1e-60:315:96//AQ153910

F-OVARC1001004//*Homo sapiens* from UWGC:y18c282 from 6p21, complete sequence.//3.1e-124:595:98//AC004190

F-OVARC1001010//CIT-HSP-2034M3.TF CIT-HSP *Homo sapiens* genomic clone 203 4M3, genomic survey sequence.//1.0:151:60//B74290

F-OVARC1001011//Human DNA sequence from cosmid U85A3, between markers DX S366 and DDX87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//3.0e-08:149:79//Z78021

F-OVARC1001032//Yeast (*S.cerevisiae*) mitochondrial Tyr-tRNA gene.//3.2e-13:667:60//M12451

F-OVARC1001034//*Mus musculus* Fn54 mRNA, partial cds.//2.5e-119:737:86//AF001533

F-OVARC1001038//*Homo sapiens* TRIAD1 type I mRNA, complete cds.//2.7e-150 :733:97//AF099149

F-OVARC1001040//*Homo sapiens* clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.8e-29:277:76//AC005081

F-OVARC1001044//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 36411, WORKING DRAFT SEQUENCE.//0.0017:387:61//AL031319

F-OVARC1001051//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.//0.012:112:74//AF053768

F-OVARC1001055//Sequence 1 from patent US 5580754.//3.3e-45:381:81//I30292

F-OVARC1001062//nbxb0026H08r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0026H08r, genomic survey sequence.//0.018:344:59//AQ271878

F-OVARC1001065//S.pombe chromosome I cosmid c29E6.//0.86:338:59//Z66525

F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.0e-130:620:98//AF082657

F-OVARC1001072//Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions.//9.3e-24:285:65//AF003529

F-OVARC1001074//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//2.0e-07:652:59//AL022153

F-OVARC1001085//Homo sapiens c-syn protooncogene mRNA, complete cds.//5.0e-35:187:99//M14333

F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone I MAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.0e-74:289:95//AJ005897

F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds.//3.6e-72:351:86//AF015913

F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//6.4e-150:710:98//AF051782

F-OVARC1001117//Homo sapiens chromosome 5, P1 clone 328E3 (LBNL H53), complete sequence.//0.99:148:67//AC005178

F-OVARC1001118//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.6e-35:302:74//AC000382

F-OVARC1001129//CIT-HSP-647P20.TP CIT-HSP Homo sapiens genomic clone 647

P20, genomic survey sequence.//0.94:106:66//B79052

F-OVARC1001154//R.norvegicus mRNA for epithelin 1 and 2.//1.8e-95:462:79  
//X62322

F-OVARC1001161//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete  
sequence.//2.9e-90:496:84//AC004069

F-OVARC1001162

F-OVARC1001167//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2  
unordered pieces.//0.00090:219:64//AC004961

F-OVARC1001169//Borrelia burgdorferi (section 27 of 70) of the complete  
genome.//1.0:265:59//AE001141

F-OVARC1001170//H.sapiens (xs170) mRNA, 350bp.//4.6e-58:355:90//Z36823

F-OVARC1001171//CIT-HSP-2285E22.TF CIT-HSP Homo sapiens genomic clone 22  
85E22, genomic survey sequence.//1.5e-25:152:83//AQ002315

F-OVARC1001173//Human DNA sequence from clone 243E7 on chromosome 22q12.  
1. Contains ESTs, STSSs and GSSs, complete sequence.//0.0024:94:80//AL022  
323

F-OVARC1001176//Streptomyces plicatus B-N-acetylhexosaminidase (hex) gene,  
complete cds.//1.0:356:60//AF063001

F-OVARC1001180//G.gallus DNA for polyubiquitin gene Ub II.//0.0062:275:6  
0//X58195

F-OVARC1001188//Homo sapiens full length insert cDNA clone ZD93F03.//1.8  
e-32:180:97//AF086486

F-OVARC1001200

F-OVARC1001232//Caenorhabditis elegans cosmid F10B5, complete sequence./  
/0.013:128:67//Z48334

F-OVARC1001240//Human Chromosome 11 pac pDJ360p17, WORKING DRAFT SEQUENC  
E, 44 unordered pieces.//3.7e-131:811:87//AC001235

F-OVARC1001243//Human BAC clone GS117010 from 7q21-q22, complete sequenc  
e.//0.044:457:59//AC003078

F-OVARC1001244//Human homolog of *Drosophila* female sterile homeotic mRNA, complete cds.//8.4e-18:118:95//M80613

F-OVARC1001261//*Mus musculus* putative membrane-associated guanylate kinase 1 (*Magi-1*) mRNA, alternatively spliced c form, partial cds.//1.4e-95:649:84//AF027505

F-OVARC1001268//*Rattus norvegicus* ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//0.00051:72:83//U35776

F-OVARC1001270

F-OVARC1001271//*Homo sapiens* mRNA for KIAA0643 protein, partial cds.//2.1e-142:644:96//AB014543

F-OVARC1001282//RPCI11-60K8.TK RPCI11 *Homo sapiens* genomic clone R-60K8, genomic survey sequence.//0.0089:285:58//AQ195857

F-OVARC1001296//*Homo sapiens* echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//3.0e-20:263:73//U97018

F-OVARC1001306//nbxb0002M13r CUGI Rice BAC Library *Oryza sativa* genomic clone nbxb0002M13r, genomic survey sequence.//0.98:170:66//AQ156061

F-OVARC1001329//*Homo sapiens* BAC clone RG370M10 from 7p15, complete sequence.//1.3e-05:432:61//AC003986

F-OVARC1001330//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.027:444:59//AC005504

F-OVARC1001339//*Homo sapiens* chromosome 17, clone hCIT.124\_H\_2, complete sequence.//0.76:89:74//AC006071

F-OVARC1001341//CITBI-E1-2503J7.TR CITBI-E1 *Homo sapiens* genomic clone 2503J7, genomic survey sequence.//0.99:45:86//AQ263402

F-OVARC1001342

F-OVARC1001344//HS-1059-A2-H02-MF.abi CIT Human Genomic Sperm Library C *Homo sapiens* genomic clone Plate=CT 781 Col=4 Row=0, genomic survey sequence.//1.5e-07:254:67//B44456

F-OVARC1001357//*Homo sapiens* Xp22-149 BAC RPCI11-46604 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.83:376:61//AC0052

97

F-OVARC1001360

F-OVARC1001369//*Homo sapiens* clone 162B15, complete sequence.//0.0066:99:76//AC004811

F-OVARC1001372//*Homo sapiens* liprin-alpha4 mRNA, partial cds.//2.7e-142:683:98//AF034801

F-OVARC1001376//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING DRAFT SEQUENCE.//1.9e-52:382:73//AL031680

F-OVARC1001381//*Homo sapiens* mRNA for candidate tumor suppressor involved in B-CLL.//1.2e-147:683:99//AJ224819

F-OVARC1001391//*S.coelicolor* whiB gene.//0.018:454:59//X62287

F-OVARC1001399//CIT-HSP-2291I8.TR CIT-HSP *Homo sapiens* genomic clone 22918, genomic survey sequence.//1.7e-11:104:87//AQ007611

F-OVARC1001417//*Homo sapiens* EXLM1 mRNA, complete cds.//3.9e-149:707:98//AB006651

F-OVARC1001419//*Homo sapiens* GOK (STIM1) mRNA, complete cds.//4.9e-48:58:69//U52426

F-OVARC1001425//Human DNA sequence from clone 1048E9 on chromosome 22q11.2-12.2 Contains pseudogene similar to ribosomal protein S3A and part of a gene similar to *C.elegans* protein CE02118, ESTs, STS, GSS, complete sequence.//0.0019:96:78//Z99714

F-OVARC1001436//*Caenorhabditis elegans* mitotic chromosome and X-chromosome associated MIX-1 protein (mix-1) mRNA, complete cds.//0.77:519:59//U96387

F-OVARC1001442//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//1.0:167:64//AL031687

F-OVARC1001453//Human DNA sequence from PAC 453D15 on chromosome 6 conta

ins STS.//4.4e-64:376:79//Z84482

F-OVARC1001476//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*

\* from clone Y24F12, WORKING DRAFT SEQUENCE.//0.20:107:71//AL022277

F-OVARC1001480

F-OVARC1001489//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.20:281:63//AC005140

F-OVARC1001496//*Homo sapiens* C-terminal binding protein 2 mRNA, complete cds.//8.1e-85:479:92//AF016507

F-OVARC1001506//*Homo sapiens* Chromosome 16 BAC clone CIT987-SKA-13F4 complete genomic sequence, complete sequence.//1.2e-98:503:83//AC002039

F-OVARC1001525//Human beta-hexosaminidase alpha chain (HEXA) gene, exon 1.//1.7e-13:87:100//M16411

F-OVARC1001542//*H.sapiens* polymorphic repeat associated with glutamate dehydrogenase pseudogene 5.//0.43:190:68//X69219

F-OVARC1001547//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.017:533:56//AC005140

F-OVARC1001555//*Homo sapiens* clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.4e-159:416:99//AC005037

F-OVARC1001577//*Homo sapiens* SRp46 splicing factor transcribed retropseudogene.//2.4e-115:540:99//AF031165

F-OVARC1001600//*Homo sapiens* chromosome 21q22.3 PAC 39C17, complete sequence.//5.5e-13:529:62//AF043945

F-OVARC1001610//, complete sequence.//1.4e-12:152:77//AC005409

F-OVARC1001611

F-OVARC1001615//Human DNA sequence from clone 873P14 on chromosome 20p12 Contains STS, GSS, complete sequence.//0.022:146:70//AL031682

F-OVARC1001668//*Homo sapiens* mRNA for MCM3 import factor, complete cds.//

/6.5e-109:358:96//AB005543

F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds.//1.8e-47:393:81//AB006867

F-OVARC1001703//CIT-HSP-2164L6.TF CIT-HSP Homo sapiens genomic clone 2164L6, genomic survey sequence.//0.94:85:69//B92840

F-OVARC1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317C6, WORKING DRAFT SEQUENCE.//1.9e-06:489:61//Z97651

F-OVARC1001713//Rattus norvegicus neuroligin 2 mRNA, complete cds.//1.0:262:59//U41662

● F-OVARC1001726//Human telomere associated repeat sequence, complete sequence.//7.5e-08:283:65//M57752

F-OVARC1001731//Mus musculus gene for beta-tropomyosin.//2.6e-83:606:81//X12650

F-OVARC1001745//HS\_3007\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=18 Row=N, genomic survey sequence.//0.00020:269:60//AQ164522

F-OVARC1001762//S.pombe chromosome III cosmid c338.//3.0e-17:624:61//AL023781

● F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//4.2e-149:706:98//U97670

F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds.//3.0e-115:580:96//AB014575

F-OVARC1001768

F-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//5.7e-64:477:78//AC005066

F-OVARC1001795//Homo sapiens chromosome 4 clone B341C20 map 4q25, complete sequence.//6.5e-11:171:76//AC004704

F-OVARC1001802//CITBI-E1-2502A17.TR CITBI-E1 Homo sapiens genomic clone 2502A17, genomic survey sequence.//0.98:214:61//AQ264481

F-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.

3-25.1. Contains the last coding exon of the gene for P18 component of a  
minoacyl-tRNA synthetase complex, part of an unknown gene downstream of  
a putative CpG island, and an STS with a CA repeat polymorphism, comple  
te sequence.//9.5e-151:712:99//AL023694

F-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial c  
ds.//2.7e-56:522:75//AF068748

F-OVARC1001812//Homo sapiens chromosome 17, clone HCIT104N19, complete s  
equence.//1.7e-63:526:81//AC003662

● F-OVARC1001813//Human DNA sequence from cosmid U144A10, between markers  
DXS366 and DXS87 on chromosome X contains STS.//0.17:214:65//Z70224

F-OVARC1001820//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 445N2, WORKING DRAFT SEQUENCE.//3.2e-55:379:82//AL031779

F-OVARC1001828//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155),  
complete sequence.//2.8e-17:509:62//AC005609

F-OVARC1001846//Human DNA sequence from cosmid U73E8, between markers DX  
S366 and DXS87 on chromosome X.//0.35:403:58//Z73361

F-OVARC1001861//CIT-HSP-2165M3.TR CIT-HSP Homo sapiens genomic clone 216  
5M3, genomic survey sequence.//2.4e-25:148:96//B94622

● F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.2e  
-18:122:95//AF070611

F-OVARC1001879//HS\_3026\_B1\_F09\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3026 Col=17 Row=L, genomic survey  
sequence.//4.9e-29:204:87//AQ207748

F-OVARC1001880//Human interferon regulatory factor 5 (Humirf5) mRNA, com  
plete cds.//3.5e-05:489:60//U51127

F-OVARC1001883//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 u  
nordered pieces.//1.9e-29:350:74//AC005020

F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homol

og (TID1) mRNA, complete cds.//8.6e-56:300:96//AF061749

F-OVARC1001901//Human DNA sequence from clone 103M22 on chromosome 6p24.

Contains STSs and GSSs, complete sequence.//2.3e-10:253:66//AL031904

F-OVARC1001911//HS\_2196\_B2\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=22 Row=P, genomic survey sequence.//3.4e-09:123:78//AQ294069

F-OVARC1001916//HS\_3054\_B1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=F, genomic survey sequence.//1.2e-31:126:97//AQ099979

● F-OVARC1001928

F-OVARC1001942//H.sapiens CpG island DNA genomic Mse1 fragment, clone 21d7, forward read cpg21d7.ft1a.//7.2e-12:83:98//Z60390

F-OVARC1001943//Aplysia californica potassium channel modulatory factor mRNA, complete cds.//3.5e-50:535:69//AF059179

F-OVARC1001949//Human KRAB zinc finger protein (ZNF177) mRNA, complete cds.//1.7e-16:294:67//U37263

F-OVARC1001950//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.5e-20:261:68//AJ011929

● F-OVARC1001987//D.melanogaster G6PD gene, exons 2-4.//0.99:447:57//Z19021

F-OVARC1001989//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//2.9e-19:178:83//AC005995

F-OVARC1002044//Plasmodium falciparum MAL3P7, complete sequence.//0.17:232:62//AL034559

F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//2.1e-158:739:98//AB007934

F-OVARC1002066//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//3.0e-17:781:59//AP000011

F-OVARC1002082//*Homo sapiens* clone DJ0965K10, WORKING DRAFT SEQUENCE, 6  
unordered pieces.//5.4e-136:683:96//AC006015

F-OVARC1002107//*Homo sapiens* BAC clone RG276003 from 7q22-q31.1, complete  
sequence.//1.0:220:61//AC004668

F-OVARC1002112//*Homo sapiens* histone macroH2A1.2 mRNA, complete cds.//6.  
1e-115:557:98//AF041483

F-OVARC1002127//*Homo sapiens* chromosome 9, clone hRPK.202\_H\_3, complete  
sequence.//0.013:461:57//AC006241

F-OVARC1002138//*Caenorhabditis elegans* cosmid F32D1.//1.0e-29:545:64//AF  
016427

F-OVARC1002143//CIT-HSP-2343H20.TR CIT-HSP *Homo sapiens* genomic clone 23  
43H20, genomic survey sequence.//2.3e-11:258:67//AQ055576

F-OVARC1002156

F-OVARC1002158//F1707-T7 IGF *Arabidopsis thaliana* genomic clone F1707, g  
enomic survey sequence.//1.8e-16:383:66//B11616

F-OVARC1002165//*H.sapiens* BDP1 mRNA for protein-tyrosine-phosphatase.//0  
.0041:300:64//X79568

F-OVARC1002182//*F.rubripes* GSS sequence, clone 123I23aA7, genomic survey  
sequence.//1.4e-10:240:66//AL017241

F-PLACE1000004//CIT-HSP-2294H13.TF CIT-HSP *Homo sapiens* genomic clone 22  
94H13, genomic survey sequence.//8.2e-10:158:75//AQ003859

F-PLACE1000005//*Mouse* alpha-1 antitrypsin gene, segment 1.//4.8e-15:89:9  
3//M12585

F-PLACE1000007//*Homo sapiens* ubiquitin hydrolyzing enzyme I (UBH1) mRNA,  
partial cds.//3.8e-51:550:72//AF022789

F-PLACE1000014

F-PLACE1000031//*Homo sapiens* clone DJ0098022, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//0.91:333:61//AC004821

F-PLACE1000040//*Homo sapiens* DNA sequence from PAC 958B3 on chromosome X

p22.11-Xp22.22. Contains ESTs STS and CpG island.//2.6e-20:279:67//Z9302

3

F-PLACE1000048//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.6e-63:488:82//AC005177

F-PLACE1000050//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141:75//U31508

F-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//1.9e-30:190:94//L22154

F-PLACE1000066//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//6.0e-63:597:74//AC005521

F-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.2e-09:143:73//AC005848

F-PLACE1000081//Human DNA from chromosome 19 specific cosmid R28461, genomic sequence, complete sequence.//0.52:390:60//AC002389

F-PLACE1000094

F-PLACE1000133//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence.//4.4e-129:731:92//AL023580

F-PLACE1000142//H.sapiens AUH mRNA.//6.4e-09:328:62//X79888

F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//7.7e-150:737:97//AF058291

F-PLACE1000185//Sequence 15 from patent US 5691147.//5.7e-106:558:94//I76211

F-PLACE1000213

F-PLACE1000214//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-06:644:57//AC005504

F-PLACE1000236//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 695020, WORKING DRAFT SEQUENCE.//2.6e-39:191:83//AL032818

F-PLACE1000246//HS\_2008\_A2\_D04\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2008 Col=8 Row=G, genomic survey sequence.//0.96:153:61//AQ269813

F-PLACE1000292//*Drosophila melanogaster* Oregon-R mitochondrial A+T region.//5.1e-12:571:60//U11584

F-PLACE1000308//*D. teissieri* mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & tRNA-Val.//0.00013:369:59//X54011

F-PLACE1000332//HS\_2016\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2016 Col=16 Row=H, genomic survey sequence.//7.5e-83:424:96//AQ232106

F-PLACE1000347//CIT-HSP-2326A16.TV CIT-HSP *Homo sapiens* genomic clone 2326A16, genomic survey sequence.//0.13:46:100//AQ047350

F-PLACE1000374//*Mus musculus* putative CCAAT binding factor 1 (mCBF) mRNA, alternatively spliced transcript mCBF1, complete cds.//0.00048:84:83//U19891

F-PLACE1000380//*F. rubripes* GSS sequence, clone 047P21aA10, genomic survey sequence.//0.43:198:62//Z88163

F-PLACE1000383//*Homo sapiens* myotubularin related protein 1 (MTMR1) mRNA, partial cds.//8.7e-149:740:96//U58032

F-PLACE1000401//*Pinctada fucata* mRNA for insoluble protein, complete cds.//0.22:484:56//D86074

F-PLACE1000406//Human nuclear matrix protein 55 (nmt55) mRNA, complete cds.//3.3e-19:372:65//U89867

F-PLACE1000420//*Homo sapiens* chromosome 17, clone hRPK.227\_G\_15, complete sequence.//1.6e-85:421:87//AC005899

F-PLACE1000421//Human GT334 protein (GT334) gene, exons 16 and 17.//0.88:145:68//U61515

F-PLACE1000424//*Homo sapiens* PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.076:196:66//AC005189

F-PLACE1000435//HS\_3217\_A2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3217 Col=24 Row=A, genomic survey sequence.//2.2e-47:438:76//AQ181698

F-PLACE1000444//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-61:616:71//AC004382

F-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//5.8e-18:314:69//AF059580

F-PLACE1000481//Homo sapiens Chromosome 22q11.2 Cosmid Clone 94a In DGCR Region, complete sequence.//1.1e-33:349:76//AC002491

F-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//1.1e-34:256:83//U35245

F-PLACE1000540//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.099:336:58//X95276

F-PLACE1000547//Arabidopsis thaliana GDP-mannose pyrophosphorylase (GMP1) mRNA, complete cds.//5.4e-11:279:63//AF076484

F-PLACE1000562//, complete sequence.//1.7e-97:559:88//AC005409

F-PLACE1000564

F-PLACE1000583//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//3.3e-46:631:68//M27877

F-PLACE1000588//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//7.3e-84:503:88//M55542

F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.8e-164:798:97//AJ012449

F-PLACE1000599//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.018:295:61//X95276

F-PLACE1000610//HS\_2056\_A1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=19 Row=G, genomic survey sequence.//5.3e-24:188:87//AQ235967

F-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.4e-47:687:66//AF044201

F-PLACE1000636

F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.5e-152:747:96//AF102265

F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)).//2.3e-156:775:97//AJ005896

F-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//8.0e-60:675  
:70//S78219

F-PLACE1000712

F-PLACE1000716//HS-1057-A1-A03-MR.abi CIT Human Genomic Sperm Library C  
Homo sapiens genomic clone Plate=CT 779 Col=5 Row=A, genomic survey sequence.//2.7e-42:266:82//B43026

F-PLACE1000748//CIT-HSP-2372J8.TR CIT-HSP Homo sapiens genomic clone 237  
2J8, genomic survey sequence.//0.023:157:68//AQ113109

F-PLACE1000749//Plasmodium falciparum MAL3P7, complete sequence.//0.099:  
664:57//AL034559

F-PLACE1000755//H.sapiens DNA 3' flanking simple sequence region clone w  
g2c3.//0.00068:206:62//X76589

F-PLACE1000769//RPCI11-3J18.TPB RPCI-11 Homo sapiens genomic clone RPCI-  
11-3J18, genomic survey sequence.//6.5e-08:93:89//B63806

F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//3.  
5e-138:663:98//AB014548

F-PLACE1000786//Drosophila melanogaster cosmid 80H7.//1.4e-43:589:68//AL  
031027

F-PLACE1000793//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13  
d12, reverse read cpg13d12.rt1c.//4.6e-09:71:100//Z64565

F-PLACE1000798//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complet

e sequence.//5.0e-14:235:72//AC002310

F-PLACE1000841//Homo sapiens clone NH0441G08, WORKING DRAFT SEQUENCE, 12  
unordered pieces.//0.013:404:60//AC006158

F-PLACE1000849//H.sapiens CpG island DNA genomic Mse1 fragment, clone 72  
a10, reverse read cpg72a10.rt1a.//3.3e-09:82:92//Z62712

F-PLACE1000856//Hydra vulgaris HT4 mRNA for collagen-like protein, parti  
al cds.//1.0:317:59//AB008935

F-PLACE1000863//H.sapiens CpG island DNA genomic Mse1 fragment, clone 53  
d2, forward read cpg53d2.ft1b.//7.3e-37:199:98//Z55621

● F-PLACE1000909//H.sapiens CpG island DNA genomic Mse1 fragment, clone 17  
3f8, reverse read cpg173f8.rt1a.//1.5e-17:128:92//Z57391

F-PLACE1000931//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1  
p35. Contains delta opiate receptor, CpG island, CA repeat,././/8.1e-55:64  
7:72//AL009181

F-PLACE1000948

F-PLACE1000972//RPCI11-61B1.TJ RPCI11 Homo sapiens genomic clone R-61B1,  
genomic survey sequence.//1.0e-26:148:99//AQ194348

● F-PLACE1000977//Homo sapiens mRNA for KIAA0672 protein, complete cds.//6  
.1e-08:413:61//AB014572

● F-PLACE1000979//H.sapiens CpG island DNA genomic Mse1 fragment, clone 76  
e8, reverse read cpg76e8.rt1a.//2.7e-10:84:94//Z55963

F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds.//8  
.0e-140:694:96//AB018267

F-PLACE1001000//Herpetomonas muscarum muscarum kinetoplast 12S rRNA gene  
.//0.0056:443:58//U01011

F-PLACE1001007//CIT-HSP-2013L15.TF CIT-HSP Homo sapiens genomic clone 20  
13L15, genomic survey sequence.//0.99:277:58//B58681

F-PLACE1001010//Human cosmid g1572c101, complete sequence.//3.6e-55:294:  
88//AC000357

F-PLACE1001015//Homo sapiens PAC clone DJ0754J18 from 7p21, complete sequence.//7.2e-33:333:73//AC004741

F-PLACE1001024

F-PLACE1001036//CIT-HSP-2373I10.TF CIT-HSP Homo sapiens genomic clone 23 73I10, genomic survey sequence.//1.1e-80:393:98//AQ108662

F-PLACE1001054//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence.//8.8e-40:483:66//AB013390

F-PLACE1001062//Mus musculus mRNA encoding lysine-ketoglutarate reductase/saccharopine dehydrogenase.//1.2e-23:224:80//AJ224761

● F-PLACE1001076//HS\_2195\_B1\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=9 Row=H, genomic survey sequence.//0.0014:168:66//AQ066659

F-PLACE1001088

F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//3.1e-9 5:489:96//AF065485

F-PLACE1001104//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.0073:253:62//U81400

F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds.//2.5e-64:676:71//AF022158

● F-PLACE1001136//Human amphiregulin (AR) gene, exon 5, clones lambda-ARH(6,12).//3.8e-26:174:93//M30702

F-PLACE1001168

F-PLACE1001171//Homo sapiens subtelomeric cosmid 11b-1, complete sequence.//7.6e-23:245:68//AC005603

F-PLACE1001185//Human DNA sequence from clone 889N15 on chromosome Xq22. 1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains

ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.010:1  
02:70//AL031177

F-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53  
) , complete cds.//9.3e-82:684:77//D14336

F-PLACE1001241

F-PLACE1001257//Caenorhabditis elegans cosmid R12E2.//1.1e-16:480:60//AF  
067219

F-PLACE1001272//H.sapiens subunit of coatomer complex.//0.31:50:96//X704  
76

● F-PLACE1001279//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 geno  
mic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.054:352:60/  
/AC005507

F-PLACE1001280//Bovine herpesvirus type 1 early-intermediate transcripti  
on control protein (BICP4) gene, complete cds.//1.0e-10:620:61//L14320

F-PLACE1001294//M.musculus GEG-154 mRNA.//5.0e-107:826:80//X71642

F-PLACE1001304//Mouse Zfp-35 mRNA for zinc finger protein ZFP-35.//1.2e-  
67:510:77//X17617

F-PLACE1001311//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4  
unordered pieces.//1.6e-47:491:73//AC005282

● F-PLACE1001323//HS-1007-A2-B10-MF.abi CIT Human Genomic Sperm Library C  
Homo sapiens genomic clone Plate=CT 328 Col=20 Row=C, genomic survey seq  
uence.//9.6e-26:142:100//B31181

F-PLACE1001351

F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds.//8.  
6e-25:155:95//AB018342

F-PLACE1001377//H.sapiens MADM gene (exon 1).//1.6e-43:393:79//Z48614

F-PLACE1001383//Human DNA sequence from clone 246H3 on chromosome 22q11.  
21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene,  
EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, c

omplete sequence.//1.5e-119:705:91//AL022324

F-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//5.7e-08  
:117:84//AJ001319

F-PLACE1001387//Sequence 3 from patent US 5610018.//1.7e-06:395:58//I573  
40

F-PLACE1001395//Plasmodium falciparum circular DNA rpoB and rpoC genes for  
beta and beta-prime subunits of RNA polymerase (EC 2.7.7.6).//7.2e-11  
:620:60//X52177

F-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING  
● DRAFT SEQUENCE, 2 ordered pieces.//3.0e-145:700:98//AC005412

F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//  
/2.0e-69:365:96//AF091087

F-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete  
sequence.//8.2e-121:608:97//AC006241

F-PLACE1001440//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE,  
8 unordered pieces.//1.3e-06:437:61//AC000384

F-PLACE1001456//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library),  
complete sequence.//0.98:348:60//AC003106

F-PLACE1001468//Homo sapiens DNA sequence from PAC 435A7 on chromosome X  
q22.1-q22.3. Contains STS.//4.4e-05:358:62//AL022148

F-PLACE1001484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
387E22, WORKING DRAFT SEQUENCE.//5.7e-31:195:93//AL031660

F-PLACE1001502//Human fibroblast growth factor receptor 3 (FGFR3) gene,  
exon 1.//0.00015:333:59//L78720

F-PLACE1001503//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)),  
complete sequence.//0.00016:161:66//AC004373

F-PLACE1001517//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-  
21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs  
.//3.7e-22:260:76//AL021786

F-PLACE1001534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//1.1e-143:713:97//AL031667

F-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence.//2.7e-139:482:96//AC005669

F-PLACE1001551//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.9e-116:681:89//AC005261

F-PLACE1001570//HS\_3105\_A1\_F06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3105 Col=11 Row=K, genomic survey sequence.//1.2e-10:137:79//AQ139817

● F-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11. //1.8e-102:217:99//AB020860

F-PLACE1001603//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//3.7e-104:501:98//AF069984

F-PLACE1001608//HS\_2189\_A1\_G07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2189 Col=13 Row=M, genomic survey sequence.//2.9e-60:429:84//AQ221959

F-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.4e-114:552:98//AC005037

● F-PLACE1001611//Human DNA sequence from clone 1039K5 on chromosome 22q12 .3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//0.93:131:71//AL031587

F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.1e-74:702:75//AB018341

F-PLACE1001634//Human p190-B (p190-B) mRNA, complete cds.//1.2e-18:114:100//U17032

F-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, complete sequence.//7.7e-159:788:97//AC005971

F-PLACE1001672//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc-Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DDXS1003 and DDXS1055, complete sequence.//7.8e-36:365:73//AL022165

F-PLACE1001691//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//9.1e-149:760:96//AC005921

● F-PLACE1001692//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds.//2.9e-57:643:71//M16200

F-PLACE1001705//Homo sapiens chromosome 17, clone hRPK.958\_E\_11, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.9e-18:284:71//AC005883

F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds.//6.6e-68:369:73//D83776

F-PLACE1001720//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31f3 In IGL C Region, complete sequence.//1.0:274:59//AC000051

F-PLACE1001729//Streptomyces coelicolor cosmid 1C2.//0.22:433:57//AL0311

24

● F-PLACE1001739//Caenorhabditis elegans cosmid C18H7.//0.049:341:61//AF067607

F-PLACE1001740//Homo sapiens chromosome 5, P1 clone 1108H7 (LBNL H81), complete sequence.//4.8e-26:372:68//AC005221

F-PLACE1001745

F-PLACE1001746//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.018:472:57//AL031744

F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//8.8e-159:773:97//AF061243

F-PLACE1001756//Homo sapiens chromosome 12p13.3 clone RPCI11-303E5, WORK

ING DRAFT SEQUENCE, 65 unordered pieces.//1.9e-54:274:81//AC005842

F-PLACE1001761//HS\_3027\_A1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=G, genomic survey sequence.//0.095:49:93//AQ130972

F-PLACE1001771//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//1.0e-146:709:97//AF080394

F-PLACE1001781

1.3e-08:238:65//AC005637

F-PLACE1001799//HS\_3075\_B1\_H03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=5 Row=P, genomic survey sequence.//1.7e-09:166:69//AQ138474

F-PLACE1001810//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone : MRC8, complete sequence.//0.00035:196:66//AB020749

F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.1e-108:546:96//AF058953

F-PLACE1001821//RPCI11-35D17.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35D17, genomic survey sequence.//2.1e-55:300:97//AQ045286

F-PLACE1001844//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//2.8e-67:443:86//AC005177

F-PLACE1001845//Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence.//0.34:219:64//AC005850

F-PLACE1001869//Klebsiella pneumoniae ribitol kinase (rbtK) and ribitol transporter (rbtT) genes, complete cds.//7.1e-11:505:57//AF045244

F-PLACE1001897//RPCI11-46D15.TJ RPCI11 Homo sapiens genomic clone R-46D15, genomic survey sequence.//9.3e-08:383:63//AQ194408

F-PLACE1001912

F-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//7.3e-156:753:98//AF099935

F-PLACE1001928//HS\_2220\_B2\_G04\_MR CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=2220 Col=8 Row=N, genomic survey sequence.//2.8e-43:233:97//AQ152361

F-PLACE1001983//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745C22, WORKING DRAFT SEQUENCE.//1.6e-07:396:62//AL031596

F-PLACE1001989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//1.0e-109:602:93//AL023755

F-PLACE1002004//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317E23, WORKING DRAFT SEQUENCE.//1.0e-69:475:87//AL020996

F-PLACE1002046//Mus musculus ligatin (Lgtn) mRNA, partial cds.//7.2e-97:623:85//U58337

F-PLACE1002052//HS\_2178\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=10 Row=H, genomic survey sequence.//4.8e-22:140:95//AQ307908

F-PLACE1002066//Apis mellifera NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.0063:371:60//U72284

F-PLACE1002072//Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A.//0.97:248:60//AF043195

F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds.//1.3e-37:635:64//AB011178

F-PLACE1002090//Homo sapiens full length insert cDNA clone ZA85C09.//7.0e-122:583:98//AF086131

F-PLACE1002115//nbxb0038A20r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0038A20r, genomic survey sequence.//0.039:210:69//AQ291086

F-PLACE1002119//Mus musculus IER5 (Ier5) mRNA, complete cds.//7.1e-61:540:77//AF079527

F-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome X q25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-125

:491:98//AL022162

F-PLACE1002150//*Plasmodium falciparum* MAL3P5, complete sequence.//0.12:4  
08:61//AL034556

F-PLACE1002157//*Homo sapiens* BAC clone NH0335J18 from 2, complete sequence.//1.1e-44:515:71//AC005539

F-PLACE1002163//*Homo sapiens* T-cell receptor alpha delta locus from base s 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.98:210:65//AE000662

F-PLACE1002170//*Homo sapiens* Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library) complete sequence.//1.2e-06:283:60//AC004805

F-PLACE1002171//*Mus musculus* interferon alpha/beta receptor (IFNAR) gene, exon 11 and partial cds.//1.0e-24:313:71//U06244

F-PLACE1002205//*Drosophila melanogaster*; Chromosome 3L; Region 79F1-80A2 ; BAC clone BACR48E05, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-05:428:60//AC005720

F-PLACE1002213//HS\_3238\_B1\_G03\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3238 Col=5 Row=N, genomic survey sequence.//2.2e-74:371:98//AQ206965

F-PLACE1002227//HS-1056-B1-C01-MF.abi CIT Human Genomic Sperm Library C *Homo sapiens* genomic clone Plate=CT 778 Col=1 Row=F, genomic survey sequence.//2.1e-07:174:71//B42800

F-PLACE1002256//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-72, complete sequence.//0.022:458:59//AL010142

F-PLACE1002259//Human DNA sequence from clone 246H3 on chromosome 22q11. 21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//3.5e-91:637:84//AL022324

F-PLACE1002319

F-PLACE1002342//*Caenorhabditis elegans* cosmid M03A1.//0.47:403:58//U4995

6

F-PLACE1002395//*Homo sapiens* chromosome 19, cosmid R28991, complete sequence.//1.9e-127:487:93//AC004623

F-PLACE1002399//*Homo sapiens* chromosome 17, clone hRPK.235\_I\_10, complete sequence.//5.6e-05:474:59//AC005922

F-PLACE1002433//*Drosophila melanogaster* fidipidine gene, exons 1-7.//1.7e-11:613:58//AJ011928

F-PLACE1002437//*M. musculus* abc1 mRNA.//5.5e-62:452:85//X75926

F-PLACE1002438//*Dictyostelium discoideum* developmental protein DG1098 (DG1098) gene, partial cds.//0.013:372:59//AF081801

F-PLACE1002450//HS\_3233\_A1\_G01\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3233 Col=1 Row=M, genomic survey sequence.//3.1e-07:449:59//AQ204769

F-PLACE1002465

F-PLACE1002474//*Mus musculus* matrilin-2 precursor mRNA, complete cds.//1.5e-110:720:85//U69262

F-PLACE1002477//*Homo sapiens* Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence.//3.9e-05:195:71//AC005926

F-PLACE1002493//*Homo sapiens* 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.020:301:60//AC006060

0

F-PLACE1002499

F-PLACE1002500//*Rattus norvegicus* zinc transporter (ZnT-2) mRNA, complete cds.//2.1e-58:465:80//U50927

F-PLACE1002514//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING DRAFT SEQUENCE.//3.7e-08:139:76//Z93930

F-PLACE1002529//*Homo sapiens* mRNA for KIAA0713 protein, partial cds.//9.0e-143:583:95//AB018256

F-PLACE1002532//*Homo sapiens* BAC clone RG300E22 from 7q21-q31.1, complete

e sequence.//0.00019:193:65//AC004774

F-PLACE1002537//Human DNA sequence from clone 127F18 on chromosome Xp11.

4-21.3. Contains part of a novel gene with some similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor Type 1 (IL1-R-1). Contains GSSs, complete sequence.//4.7e-25:198:84//AL03 1575

F-PLACE1002571//Drosophila melanogaster actin-related protein mRNA, complete cds.//2.0e-13:400:60//L25314

F-PLACE1002578//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//3.5e-11:167:72//AC002523

F-PLACE1002583//Mus musculus glutamate receptor subunit (GluR6) gene, partial cds.//4.2e-09:370:61//U31443

F-PLACE1002591//H.sapiens mRNA for coronin.//7.2e-26:279:74//X89109

F-PLACE1002598//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.0013:375:64//AC005537

F-PLACE1002604//Hansenula wingei mitochondrial DNA, complete sequence.//4.7e-05:556:59//D31785

F-PLACE1002625

F-PLACE1002655//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.6e-128:229:92//AC005281

F-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//3.6e-107:706:84//AF079765

F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//3.4e-186:804:97//AF068180

F-PLACE1002714//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//2.3e-16:474:64//AF051726

F-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-107:552:95//I73 723

F-PLACE1002768//Human DNA sequence from clone 726F20 on chromosome 1p36.

11-36.23. Contains ESTs and a GSS, complete sequence.//0.0076:161:70//AL

031273

F-PLACE1002772//HS\_3058\_A1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=3 Row=G, genomic survey sequence.//0.0046:192:64//AQ134567

F-PLACE1002775//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//7.6e-14:459:62//AF084259

F-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.6e-43:385:77//U50927

● F-PLACE1002794//CIT-HSP-2368A17.TR CIT-HSP Homo sapiens genomic clone 23 68A17, genomic survey sequence.//1.3e-71:368:96//AQ075879

F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds.//1.8e-44:567:70//D79994

F-PLACE1002815//Sequence 25 from patent US 5747660.//2.6e-07:150:73//AR0 05295

F-PLACE1002816//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds .//1.3e-68:687:73//AF039691

● F-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//9.3e-41:240:93//M27877

● F-PLACE1002839//Human BAC clone RG205G13 from 7q31, complete sequence.//0.00087:213:63//AC003045

F-PLACE1002851//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0032:269:6 6//AC005140

F-PLACE1002853//Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete transcribed region and flanks.//0.032:275:62 /M10126

F-PLACE1002881//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING DRAFT SEQUENCE.//4.7e-38:355:76//Z98200

F-PLACE1002908//*Gallus gallus* beta-1,4-galactosyltransferase (CKII) mRNA, complete cds.//0.00012:200:64//U19889

F-PLACE1002941//Human BAC clone RG161K23 from 7q21, complete sequence.//1.1e-14:241:70//AC000120

F-PLACE1002962

F-PLACE1002968//*Plasmodium falciparum* MAL3P2, complete sequence.//0.21:410:59//AL034558

F-PLACE1002991//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//6.8e-121:605:93//AL023755

F-PLACE1002993//CIT-HSP-2338I16.TF CIT-HSP *Homo sapiens* genomic clone 238I16, genomic survey sequence.//1.9e-13:100:95//AQ054760

F-PLACE1002996//Mouse U6 RNA gene.//2.0e-13:113:90//X06980

F-PLACE1003025//*Plasmodium falciparum* MAL3P6, complete sequence.//0.84:374:58//Z98551

F-PLACE1003027//*Homo sapiens* mRNA for KIAA0516 protein, partial cds.//6.1e-130:632:97//AB011088

F-PLACE1003044//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.6e-123:687:91//E12829

F-PLACE1003045//*H.sapiens* CpG island DNA genomic Mse1 fragment, clone 47g6, forward read cpg47g6.ft1a.//0.0064:52:96//Z61200

F-PLACE1003092//CIT-HSP-387P22.TRB CIT-HSP *Homo sapiens* genomic clone 387P22, genomic survey sequence.//0.0031:249:63//B60158

F-PLACE1003100//Human Hep27 protein mRNA, complete cds.//8.9e-65:650:73//U31875

F-PLACE1003108

F-PLACE1003136//*Homo sapiens* chromosome 5, P1 clone 1130f1 (LBNL H40), complete sequence.//6.3e-46:606:68//AC004219

F-PLACE1003145

F-PLACE1003153//RPCI11-13P16.TP RPCI-11 *Homo sapiens* genomic clone RPCI-

11-13P16, genomic survey sequence.//2.7e-63:478:82//B76206  
F-PLACE1003174//Human DNA sequence from clone 441J1 on chromosome 6p24 C  
ontains STS, GSS, complete sequence.//0.61:147:65//Z99495  
F-PLACE1003176//HS\_2255\_A2\_B01\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2255 Col=2 Row=C, genomic survey s  
equence.//6.3e-09:137:76//AQ131934  
F-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 u  
nordered pieces.//2.4e-138:791:90//AC005095  
F-PLACE1003200//P.falciparum complete gene map of plastid-like DNA (IR-B  
).//8.7e-06:728:57//X95276  
F-PLACE1003205//Human BAC clone RG354L07 from 7q31, complete sequence.//  
7.5e-05:249:63//AC002466  
F-PLACE1003238//HS\_3239\_A2\_G02\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3239 Col=4 Row=M, genomic survey s  
equence.//0.36:64:87//AQ209954  
F-PLACE1003249  
F-PLACE1003256  
F-PLACE1003258//HS\_3223\_A1\_G10\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3223 Col=19 Row=M, genomic survey  
sequence.//1.4e-07:227:65//AQ190317  
F-PLACE1003296//CIT-HSP-2337F11.TF CIT-HSP Homo sapiens genomic clone 23  
37F11, genomic survey sequence.//1.1e-13:97:95//AQ057429  
F-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of  
HPF1, -2, and -9.//2.3e-92:485:95//M27877  
F-PLACE1003334  
F-PLACE1003342  
F-PLACE1003343//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14  
unordered pieces.//1.0e-20:179:84//AC004951  
F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 pro

tein (BCAR3) mRNA, complete cds.//8.0e-143:773:92//U92715  
F-PLACE1003361//Human Cosmid g1248a143 from 7q31.3, complete sequence.//  
1.9e-30:402:70//AC004095  
F-PLACE1003366  
F-PLACE1003369//Plasmodium falciparum MAL3P2, complete sequence.//7.6e-0  
7:378:60//AL034558  
F-PLACE1003373//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete  
sequence.//6.0e-18:471:61//AC005247  
F-PLACE1003375  
● F-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat e  
pithelium cancer , segment 10/10.//2.3e-157:779:96//AB020878  
F-PLACE1003394//Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.//  
1.2e-104:596:91//M83680  
F-PLACE1003401//RPCI11-71J5.TJ RPCI11 Homo sapiens genomic clone R-71J5,  
genomic survey sequence.//0.85:140:65//AQ268588  
F-PLACE1003420//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y1E3, WORKING DRAFT SEQUENCE.//0.0015:286:60//AL021388  
F-PLACE1003454//Plasmodium falciparum microsatellite pe63 sequence.//0.0  
084:219:61//AF015470  
● F-PLACE1003478//Homo sapiens calcium-dependent chloride channel-1 (hCLCA  
1) gene, complete cds.//1.3e-11:746:60//AF039401  
F-PLACE1003493  
F-PLACE1003516//Homo sapiens chromosome 17, clone HRPC987K16, complete s  
equence.//8.2e-41:379:78//AC002994  
F-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequ  
ence, containing ribosomal protein homologue pseudogene L23a.//6.2e-21:2  
47:76//AF064859  
F-PLACE1003521//Human DNA sequence from PAC 257A7 on chromosome 6p24. Co  
ntains two unknown genes and ESTs, STSs and a GSS.//4.4e-68:502:79//AL00

8729

F-PLACE1003528//*Homo sapiens* DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//1.0:323:58//AL022336

F-PLACE1003537//*Homo sapiens* multispanning membrane protein mRNA, complete cds.//0.0054:322:59//U94831

F-PLACE1003553//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-78:267:88//AL031297

F-PLACE1003566//*Plasmodium falciparum* MAL3P3, complete sequence.//0.00026:514:58//Z98547

F-PLACE1003575//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.079:755:54//AC004688

F-PLACE1003583//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.1e-41:212:74//AL022324

F-PLACE1003584//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-56, complete sequence.//0.0038:465:57//AL010230

F-PLACE1003592//*Homo sapiens* chromosome 17, clone 296K1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.72:111:71//AC002557

F-PLACE1003593//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.096:162:66//AC002476

F-PLACE1003596//*Mus musculus* integral membrane protein 1 (Itm1) mRNA, complete cds.//1.4e-54:685:68//L34260

F-PLACE1003602//*Homo sapiens* mRNA expressed in placenta.//1.1e-138:679:97//D83200

F-PLACE1003605//*Homo sapiens* chromosome 16, cosmid clone RT81 (LANL), co

plete sequence.//0.0074:265:63//AC005356

F-PLACE1003611//HS\_2198\_B1\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2198 Col=3 Row=H, genomic survey sequence.//2.1e-23:137:97//AQ184475

F-PLACE1003618//Homo sapiens chromosome 4 clone C0011C13 map 4p16, complete sequence.//3.0e-122:725:89//AC006226

F-PLACE1003625//HS\_2238\_B2\_D11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=22 Row=H, genomic survey sequence.//4.8e-12:92:94//AQ065662

● F-PLACE1003638//Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone : MKD10, complete sequence.//0.043:264:63//AB011478

F-PLACE1003669

F-PLACE1003704//RPCI11-23H21.TKBF RPCI-11 Homo sapiens genomic clone RPC I-11-23H21, genomic survey sequence.//7.1e-31:199:91//AQ013830

F-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//4.3e-132:669:95//AF053305

F-PLACE1003711//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1 p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//1.5e-31:166:99//AL021920

● F-PLACE1003723//HS\_2231\_A2\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=14 Row=E, genomic survey sequence.//1.2e-12:114:90//AQ235672

F-PLACE1003738//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//5.9e-33:592:67//M58297

F-PLACE1003760//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//3.6e-11:92:93//AF054840

F-PLACE1003762

F-PLACE1003768//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 7/15, WORKING DRAFT SEQUENCE.//4.8e-77:737:76//AP00

0014

F-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//2.1e-164:793:98//AC004160

F-PLACE1003783//HS\_2190\_A2\_C02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=4 Row=E, genomic survey sequence.//1.1e-26:147:100//AQ218757

F-PLACE1003784//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//4.5e-57:706:68//AC006210

F-PLACE1003795//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene.//0.015:296:60//U52112

F-PLACE1003833//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//0.52:212:64//AL022339

F-PLACE1003850//P.falciparum histidine-rich protein genes.//0.39:330:60//M17028

F-PLACE1003858//Human DNA sequence from PAC 332011 on chromosome 1q24-1q25. Contains ESTs and STSs.//4.8e-07:461:59//Z98043

F-PLACE1003864//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.026:538:56//AC005139

F-PLACE1003870//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//6.5e-06:175:69//Z98304

F-PLACE1003885//Mus musculus poly(A) polymerase VI mRNA, complete cds.//9.4e-75:754:72//U58134

F-PLACE1003886//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.7e-20:432:64//AC006030

F-PLACE1003888//Human mRNA for phospholipase C, complete cds.//2.6e-53:7  
02:67//D42108

F-PLACE1003892//RPCI11-24P17.TV RPCI-11 Homo sapiens genomic clone RPCI-  
11-24P17, genomic survey sequence.//3.3e-20:245:65//B86759

F-PLACE1003900//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 328E19, WORKING DRAFT SEQUENCE.//2.5e-17:260:71//AL022240

F-PLACE1003903//Mus musculus CTP synthetase homolog (CTPSH) mRNA, comple  
te cds.//2.7e-86:533:87//U49385

F-PLACE1003915//Mus musculus clone OST1963, genomic survey sequence.//6.  
4e-29:251:80//AF046591

F-PLACE1003923//Homo sapiens full length insert cDNA clone ZD40A05.//2.8  
e-25:316:70//AF086251

F-PLACE1003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic  
sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.6e-05:652:58//  
AC005505

F-PLACE1003936//CIT-HSP-2387C11.TR.1 CIT-HSP Homo sapiens genomic clone  
2387C11, genomic survey sequence.//1.0:223:62//AQ239494

F-PLACE1003968//Rattus norvegicus 5'-AMP-activated protein kinase, gamma  
-1 subunit mRNA, complete cds.//5.2e-47:505:72//U42413

F-PLACE1004103//Homo sapiens chromosome 19, cosmid R28784, complete sequ  
ence.//6.7e-29:241:84//AC005954

F-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//3.0e-115:71  
9:86//AF032666

F-PLACE1004114//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Re  
gion, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.5e-22:213:80//AC000  
052

F-PLACE1004118//Pseudorabies virus with upstream and downstream sequences  
.//0.87:209:64//M34651

F-PLACE1004128//M.musculus G protein beta-subunit mRNA, complete cds.//2

.5e-62:437:84//M63658

F-PLACE1004149//Oryctolagus cuniculus translation initiation factor eIF2  
C mRNA, complete cds.//1.4e-16:342:65//AF005355

F-PLACE1004156//Homo sapiens DNA sequence from PAC 57E3 on chromosome 6p  
12.1-21.1. Contains GSSs and an STS with a TATC repeat polymorphism, com  
plete sequence.//1.2e-26:299:74//AL022099

F-PLACE1004161

F-PLACE1004183//Homo sapiens for TOM1-like protein.//1.2e-146:731:96//AJ  
010071

F-PLACE1004197

F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precur  
sor, mRNA, complete cds.//4.0e-144:695:98//AF069493

F-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6  
q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA rep  
eat polymorphism, complete sequence.//2.3e-151:772:95//AL021326

F-PLACE1004256//HS\_2010\_B2\_G04\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2010 Col=8 Row=N, genomic survey s  
equence.//1.5e-44:372:79//AQ252434

F-PLACE1004257//Homo sapiens BAC clone NH0342K06 from 2, complete sequen  
ce.//0.00011:349:63//AC005034

F-PLACE1004258//Homo sapiens DNA sequence from PAC 779B17 on chromosome  
22q13.1. Contains exon trap, complete sequence.//0.77:475:59//AL021806

F-PLACE1004270//Human IgA C alpha 1 switch region (Sa1).//1.7e-08:622:61  
//L19121

F-PLACE1004274//H.sapiens CpG island DNA genomic Mse1 fragment, clone 18  
g6, forward read cpg18g6.ft1b.//8.6e-37:196:98//Z57691

F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, c  
omplete cds.//6.0e-156:756:97//AF084830

F-PLACE1004284//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone

: MPI7, complete sequence.//0.0060:635:57//AB011480

F-PLACE1004289//HS\_3023\_B1\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=7 Row=J, genomic survey sequence.//2.4e-12:86:98//AQ094451

F-PLACE1004302//Streptomyces coelicolor cosmid 7H1.//0.26:297:64//AL0214  
11

F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//2.9e-150  
:797:94//Y11588

F-PLACE1004336//Drosophila melanogaster DNA sequence (P1 DS07968 (D117))  
, complete sequence.//0.87:206:59//AC004267

F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1  
mRNA, complete cds.//5.9e-139:688:97//AF100153

F-PLACE1004376//Mus musculus clone OST20307, genomic survey sequence.//4  
.1e-81:498:89//AF046631

F-PLACE1004384//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 1121J18, WORKING DRAFT SEQUENCE.//3.6e-41:482:73//AL031653

F-PLACE1004388//Caenorhabditis elegans cosmid K08F11.//8.6e-26:615:62//U  
70855

F-PLACE1004405//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 u  
nordered pieces.//9.2e-150:749:96//AC005027

F-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete  
sequence.//2.4e-08:129:76//AC005532

F-PLACE1004428//R.norvegicus mRNA for Pristanoyl-CoA Oxidase.//7.0e-17:5  
49:61//X95188

F-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit  
precursor, mRNA, nuclear gene encoding mitochondrial protein, complete  
cds.//3.1e-129:536:99//U49283

F-PLACE1004451//Human DNA sequence from PAC 214K23, BRCA2 gene region ch  
romosome 13q12-13 contains BRCA2 exons 1-24, Interferon Induced 56Kd pse

udogene and ESTs.//4.8e-23:231:71//Z74739

F-PLACE1004460//*Homo sapiens* PAC clone DJ1064B22 from 7q21, complete sequence.//0.96:454:56//AC004954

F-PLACE1004467//HS\_2058\_B1\_C09\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2058 Col=17 Row=F, genomic survey sequence.//2.4e-87:433:98//AQ242700

F-PLACE1004471//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-74:665:70//M27877

F-PLACE1004473//CIT-HSP-2045A15.TF CIT-HSP *Homo sapiens* genomic clone 2045A15, genomic survey sequence.//3.3e-20:140:92//B80243

F-PLACE1004491//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.9e-05:794:57//AC004709

F-PLACE1004506//Human Gx-alpha gene.//1.0e-05:231:63//D90150

F-PLACE1004510//*Homo sapiens* TATA binding protein associated factor (TAF II150) mRNA, complete cds.//3.2e-146:699:98//AF040701

F-PLACE1004516//Human DNA sequence from cosmid SRL9A13, chromosome region 11p13. Contains EST.//1.4e-33:367:71//Z86001

F-PLACE1004518

F-PLACE1004548//*Dictyostelium discoideum* MigA (migA) gene, complete cds.//2.6e-05:318:62//U86962

F-PLACE1004550//Human FMR1 gene, 5' end.//0.0018:142:66//L19476

F-PLACE1004564//*B. taurus* mRNA for cleavage and polyadenylation specificity factor.//1.7e-114:513:85//X75931

F-PLACE1004629//*Anolis carolinensis* Brain-1 gene, complete cds.//0.00013:188:67//AB001868

F-PLACE1004645//*Mycobacterium tuberculosis* H37Rv complete genome; segment 138/162.//0.66:337:60//Z95120

F-PLACE1004646//*Rattus norvegicus* retinal pigment epithelium-specific pr

otein (Rpe65) mRNA, complete cds.//1.1e-19:326:63//AF035673  
F-PLACE1004658//H.sapiens CpG island DNA genomic Mse1 fragment, clone 55  
h1, forward read cpg55h1.ft1a.//2.4e-34:188:98//Z61632  
F-PLACE1004664//Caenorhabditis elegans cosmid W10G6, complete sequence./  
/1.0:148:65//Z81140  
F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M860  
4 Met protein (M8604 Met) gene, complete cds.//1.9e-101:182:95//U07561  
F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, compl  
ete cds.//4.3e-109:625:91//AF035606  
● F-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of  
hepatocellular colorectal and non-small cell lung cancer , segment 3/11.  
//1.9e-152:759:96//AB020860  
F-PLACE1004686//Homo sapiens DNA sequence from PAC 179N16 on chromosome  
6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternati  
vely spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MA  
PK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islan  
ds, complete sequence.//1.2e-34:320:71//Z95152  
● F-PLACE1004691//HS\_3044\_A1\_G01\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3044 Col=1 Row=M, genomic survey s  
equence.//0.018:191:63//AQ098323  
F-PLACE1004693//Human DNA sequence from clone 353H6 on chromosome Xq25-2  
6.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related  
, matrix associated, actin dependent regulator of chromatin, subfamily a  
, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains  
ESTs, STSs and GSSs, complete sequence.//0.28:573:57//AL022577  
F-PLACE1004716//Plasmodium falciparum MAL3P6, complete sequence.//0.0008  
1:428:59//Z98551  
F-PLACE1004722//HS\_3052\_B1\_C10\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3052 Col=19 Row=F, genomic survey

sequence.//2.3e-05:104:75//AQ134959

F-PLACE1004736//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 23  
65J21, genomic survey sequence.//1.3e-24:180:88//AQ080498

F-PLACE1004740//RPCI11-58A7.TJ RPCI11 Homo sapiens genomic clone R-58A7,  
genomic survey sequence.//8.6e-26:522:65//AQ195766

F-PLACE1004743//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA,  
complete cds.//1.1e-112:711:86//AF061555

F-PLACE1004751

F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//5.4e-  
171:828:97//AF084367

F-PLACE1004777//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7./  
/4.2e-134:763:90//AJ001713

F-PLACE1004793//Human DNA sequence from clone 323P24 on chromosome Xp11.  
21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34), hypothetical protein  
EST, STS, GSS, complete sequence.//9.3e-132:759:90//AL022157

F-PLACE1004804

F-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic  
sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.5e-06:403:58//  
AC004710

F-PLACE1004814//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete  
sequence.//9.8e-39:207:99//AC005921

F-PLACE1004815//Homo sapiens PAC clone DJ0651K02 from 7p21-p22, complete  
sequence.//8.1e-15:203:73//AC004613

F-PLACE1004824//G.gallus PB1 gene.//1.1e-103:759:80//X90849

F-PLACE1004827//HS\_2230\_A2\_A05\_MR CIT Approved Human Genomic Sperm Library D  
Homo sapiens genomic clone Plate=2230 Col=10 Row=A, genomic survey  
sequence.//4.1e-38:330:81//AQ299313

F-PLACE1004836//H.sapiens nidogen gene (exon 8).//0.97:116:68//X84825

F-PLACE1004838//HS\_3241\_A2\_A04\_MR CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=3241 Col=8 Row=A, genomic survey sequence.//1.8e-87:425:98//AQ206740

F-PLACE1004840//Sequence 2 from patent US 5728819.//6.7e-47:285:91//I928  
19

F-PLACE1004868

F-PLACE1004885//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 9.//0.14:465:59//Z97344

F-PLACE1004900

F-PLACE1004902//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2  
510J4, genomic survey sequence.//3.6e-06:56:100//AQ261184

F-PLACE1004913//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.6e-151:770:91//AC005058

F-PLACE1004918//Mus musculus signaling molecule (ATTP) mRNA, complete cds.//2.6e-68:459:84//U97571

F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//4.4e-106:545:95//AF070671

F-PLACE1004934//Human DNA sequence from clone 192P9 on chromosome Xp11.2  
3-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs,  
complete sequence.//3.5e-45:226:84//AL020989

F-PLACE1004937

F-PLACE1004969

F-PLACE1004972//Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete sequence.//0.012:316:61//AC004843

F-PLACE1004979//Human DNA sequence from clone 142F18 on chromosome Xq26.  
3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST,  
GSS and an inverted repeat, complete sequence.//4.7e-39:394:77//AL03  
1073

F-PLACE1004982//Caenorhabditis elegans cosmid B0507.//0.16:167:65//U6483

F-PLACE1004985//*Plasmodium falciparum* chromosome 2, section 10 of 73 of the complete sequence.//8.8e-14:590:61//AE001373

F-PLACE1005026

F-PLACE1005027

F-PLACE1005046

F-PLACE1005052//*Homo sapiens* chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//2.1e-135:675:97//AC005867

F-PLACE1005055//*Homo sapiens* mRNA for KIAA0576 protein, partial cds.//1.

9e-159:761:98//AB011148

● F-PLACE1005066//*Homo sapiens* actin binding protein MAYVEN mRNA, complete cds.//9.2e-10:757:56//AF059569

F-PLACE1005077

F-PLACE1005085//*Homo sapiens* Xp22-132-134 BAC GSHB-590J15 (Genome System Human BAC library) complete sequence.//6.9e-29:253:77//AC004673

F-PLACE1005086//*Homo sapiens* chromosome 17, clone HCIT11023, complete sequence.//6.5e-52:446:78//AC002316

F-PLACE1005101//*Homo sapiens* clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.0e-146:734:96//AC005225

● F-PLACE1005102//*Homo sapiens* chromosome 19, cosmid R29388, complete sequence.//9.8e-83:254:95//AC004476

F-PLACE1005108//Human BAC clone RG009H02 from 7q31, complete sequence.//0.46:179:64//AC003081

F-PLACE1005111

F-PLACE1005128//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.00051:287:63//L14320

F-PLACE1005146//HS\_3071\_A1\_E03\_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3071 Col=5 Row=I, genomic survey sequence.//7.4e-38:299:82//AQ103361

F-PLACE1005162//Human BAC clone GS306C12 from 7q21-q22, complete sequence

e.//2.6e-44:346:82//AC002451

F-PLACE1005176

F-PLACE1005181//CIT-HSP-234005.TR CIT-HSP Homo sapiens genomic clone 234  
005, genomic survey sequence.//0.99:211:63//AQ054651

F-PLACE1005187//CIT-HSP-2358N6.TR CIT-HSP Homo sapiens genomic clone 235  
8N6, genomic survey sequence.//2.7e-07:80:90//AQ074445

F-PLACE1005206//Human BAC clone 133K23 from 7q31.2, complete sequence.//  
0.98:216:61//AC000061

F-PLACE1005232//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42  
unordered pieces.//0.70:245:63//AC004965

F-PLACE1005243

F-PLACE1005261//Caenorhabditis elegans cosmid T05H10, complete sequence.  
//0.00041:254:61//Z47812

F-PLACE1005266//H.sapiens mRNA (fetal brain cDNA a4\_2g).//9.6e-33:177:98  
//Z70695

F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.  
6e-148:706:98//AB011182

F-PLACE1005287//Plasmodium falciparum (MESA) mRNA exons 1-2, complete cd  
s.//2.8e-15:737:60//M69183

F-PLACE1005305//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, co  
mplete cds.//3.8e-111:728:84//M25757

F-PLACE1005308//Clethrionomys glareolus endogenous retroviral sequence E  
RV-L pol gene, clone ERV-L Vole Cg14.//1.0:128:67//AJ233621

F-PLACE1005313//Caenorhabditis elegans cosmid D2092.//8.8e-11:342:62//U8  
8167

F-PLACE1005327//HS\_3080\_B2\_A12\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3080 Col=24 Row=B, genomic survey  
sequence.//4.1e-25:147:96//AQ139116

F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequ

ence.//1.4e-132:399:94//AC004794

F-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE,  
2 unordered pieces.//5.5e-114:237:92//AC000380

F-PLACE1005373

F-PLACE1005374//Homo sapiens chromosome 7 common fragile site, complete  
sequence.//0.20:305:58//AF017104

F-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//  
2.5e-148:760:95//AC003991

F-PLACE1005453//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
\* from clone Y48A6, WORKING DRAFT SEQUENCE.//0.00069:582:59//Z92854

F-PLACE1005467//Rat mRNA.//0.0014:131:70//M59859

F-PLACE1005471//Human DNA sequence from clone 45I4 on chromosome 6q24.1-  
24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete  
sequence.//3.0e-23:530:67//AL023581

F-PLACE1005477//Human DNA sequence from clone J181N11, WORKING DRAFT SEQ  
UENCE.//3.3e-131:814:88//Z82191

F-PLACE1005480//Homo sapiens DNA sequence from PAC 257I20 on chromosome  
22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP  
2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repea  
t, STS, GSS.//7.0e-34:246:73//AL021878

F-PLACE1005481//RPCI11-74L17.TJ RPCI11 Homo sapiens genomic clone R-74L1  
7, genomic survey sequence.//0.37:403:57//AQ266885

F-PLACE1005494//Homo sapiens transient receptor potential protein 6 mRNA  
, complete cds.//2.1e-67:325:99//AF080394

F-PLACE1005502//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete  
sequence.//0.015:403:61//AC005589

F-PLACE1005526//H.sapiens CpG island DNA genomic Msel fragment, clone 9f  
1, reverse read cpg9f1.rt1a.//3.6e-27:159:96//Z66485

F-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/

28, WORKING DRAFT SEQUENCE.//2.6e-28:449:67//AP000038

F-PLACE1005530//*Homo sapiens* clone DJ0691L07, complete sequence.//6.5e-1  
8:234:72//AC004860

F-PLACE1005550//*Fugu rubripes* GSS sequence, clone 048A08bH3, genomic sur  
vey sequence.//1.2e-14:123:75//AL025925

F-PLACE1005554//*Leishmania tarentolae* mitochondrial 12S ribosomal RNA ge  
ne.//0.43:209:66//X02354

F-PLACE1005557//*Homo sapiens* chromosome 17, clone hRPC.117\_B\_12, complet  
e sequence.//9.3e-113:536:97//AC004707

F-PLACE1005574//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1383 genomi  
c sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-10:514:59/  
/AC005504

F-PLACE1005584//*Homo sapiens* mRNA for KIAA0617 protein, complete cds.//0  
.00056:289:63//AB014517

F-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete se  
quence.//1.2e-111:262:89//AC004126

F-PLACE1005603

F-PLACE1005611//F1605TFC IGF *Arabidopsis thaliana* genomic clone F1605, g  
enomic survey sequence.//2.0e-10:209:66//B98589

F-PLACE1005623

F-PLACE1005630//High throughput sequencing of human chromosome 12, WORKI  
NG DRAFT SEQUENCE, 1 ordered pieces.//1.2e-93:230:98//AC005840

F-PLACE1005639//HS\_3095\_B1\_A03\_MF CIT Approved Human Genomic Sperm Libra  
ry D *Homo sapiens* genomic clone Plate=3095 Col=5 Row=B, genomic survey s  
equence.//1.2e-05:220:63//AQ123022

F-PLACE1005646//*Homo sapiens* RNA helicase-related protein mRNA, complete  
cds.//6.4e-150:721:98//AF083255

F-PLACE1005656//*H.sapiens* RR2 mRNA for small subunit ribonucleotide redu  
ctase.//1.3e-51:480:74//X59618

F-PLACE1005666//RPCI11-78015.TV RPCI11 Homo sapiens genomic clone R-78015, genomic survey sequence.//8.7e-05:243:62//AQ284667

F-PLACE1005698//Human membrane-associated lectin type-C mRNA.//1.9e-63:374:85//M98457

F-PLACE1005727//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.69:633:57//AE001422

F-PLACE1005730//HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//2.0e-24:286:74//AQ231147

● F-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds.//2.8e-55:621:71//U15635

F-PLACE1005755//HS\_2213\_A2\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=22 Row=0, genomic survey sequence.//1.4e-25:290:75//AQ136844

F-PLACE1005763//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds.//4.5e-40:297:70//M16200

F-PLACE1005799//R.norvegicus mRNA for mitochondrial isoform of cytochrome b5.//0.91:287:63//Y12517

● F-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//5.0e-109:530:98//AC004827

F-PLACE1005803//HS\_3092\_B1\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=19 Row=B, genomic survey sequence.//2.4e-08:76:96//AQ103695

F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.4e-126:636:96//AF027156

F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//2.6e-154:739:98//AF065482

F-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.2e-37:355:77//AC004150

F-PLACE1005834//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from contig 4-105, complete sequence.//0.00080:663:58//AL010283

F-PLACE1005845//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC812 genomic  
sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00015:340:58//  
AC004153

F-PLACE1005850//Human DNA sequence from clone 465N24 on chromosome 1p35.  
1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete  
sequence.//1.8e-46:278:85//AL031432

F-PLACE1005851

F-PLACE1005876//*B. taurus* mRNA for cleavage and polyadenylation specifici  
ty factor.//5.0e-120:701:89//X75931

F-PLACE1005884//CIT-HSP-2333012.TR CIT-HSP *Homo sapiens* genomic clone 23  
33012, genomic survey sequence.//4.6e-78:385:98//AQ039226

F-PLACE1005890//*Schizosaccharomyces pombe* *bem1/bud5* suppressor (Bem46+)  
mRNA, partial cds.//9.3e-16:638:57//U29892

F-PLACE1005898//*Rattus norvegicus* A-kinase anchoring protein AKAP150 mRNA  
A, complete cds.//1.0:178:65//U67136

F-PLACE1005921//*M. musculus* mRNA for immunity associated protein 38.//6.6  
e-17:614:59//Y08026

F-PLACE1005923//RPCI11-33G19.TJ RPCI-11 *Homo sapiens* genomic clone RPCI-  
11-33G19, genomic survey sequence.//4.0e-10:535:57//AQ046151

F-PLACE1005925//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 537K23, WORKING DRAFT SEQUENCE.//0.17:159:65//AL034405

F-PLACE1005932

F-PLACE1005934//*H. sapiens* CpG island DNA genomic *MseI* fragment, clone 16  
5g2, forward read *cpg165g2.ft1a*.//8.3e-43:247:93//Z57153

F-PLACE1005936//*F. rubripes* GSS sequence, clone 069K22aG2, genomic survey  
sequence.//0.91:116:68//AL014719

F-PLACE1005951//*Rhodobacter sphaeroides* DMSO/TMAO-sensor kinase (*dorS*),

DMSO/TMAO-response regulator (dorR), DMSO/TMAO-cytochrome c-containing subunit (dorC), DMSO-membrane protein (dorB), and DMSO/TMAO-reductase (dorA) genes, complete cds.//0.0022:495:59//AF016236

F-PLACE1005953//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.9e-05:442:61//AC004081

F-PLACE1005955//Caenorhabditis elegans cosmid F01F1.//4.3e-20:409:64//U13070

F-PLACE1005966//P.falciparum aarp3 gene, exon.//0.0083:270:64//Y08925

F-PLACE1005968

F-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//1.0e-100:513:96//AC005866

F-PLACE1006002//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//2.5e-54:444:77//Z86090

F-PLACE1006003//HS-1059-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=2 Row=M, genomic survey sequence.//3.4e-05:214:64//B44442

F-PLACE1006011//Mus musculus poly-(ADPribosyl)-transferase homolog PARP mRNA, complete cds.//4.3e-71:580:79//AF072521

F-PLACE1006017//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 complete genomic sequence, complete sequence.//8.6e-32:177:83//AC002299

F-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//1.8e-34:269:83//U01139

F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//3.4e-147:719:97//X99906

F-PLACE1006076//Homo sapiens DNA sequence from PAC 79C4 on chromosome 1q 24. Contains the PMX1 gene, coding for two alternative forms of the Paired Mesoderm Homeobox protein 1 (PMX-1, PHOX-1). Contains ESTs, STSSs and BAC end sequences (GSSs), complete sequence.//0.37:332:62//Z97200

F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds./

/1.3e-145:679:99//AF039023

F-PLACE1006129

F-PLACE1006139//*Saccharomyces cerevisiae* chromosome VI cosmid 9965.//4.8  
e-27:693:60//D44597

F-PLACE1006143//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 169I5, WORKING DRAFT SEQUENCE.//4.7e-46:435:77//Z93015

F-PLACE1006157//*Saguinus oedipus* mRNA for membrane cofactor protein CD46  
, complete cds, clone:B2.//0.048:290:60//D85750

F-PLACE1006159//*Homo sapiens* chromosome 10 clone CIT987SK-105402 map 10q  
25, complete sequence.//3.2e-129:466:96//AC005661

F-PLACE1006164//HS\_3003\_A1\_F08\_MR CIT Approved Human Genomic Sperm Libra  
ry D *Homo sapiens* genomic clone Plate=3003 Col=15 Row=K, genomic survey  
sequence.//1.4e-70:388:93//AQ118200

F-PLACE1006167//*Homo sapiens* chromosome 19, cosmid F23149, complete sequ  
ence.//4.3e-78:385:86//AC005239

F-PLACE1006170//Mouse mRNA for alpha-adaptin (C).//3.5e-91:630:84//X1497  
2

F-PLACE1006187//*Homo sapiens* cyclin E2 mRNA, complete cds.//3.9e-149:694  
:99//AF091433

F-PLACE1006195//*Homo sapiens* Xp22 BAC GS-607H18 (Genome Systems Human BA  
C library) complete sequence.//2.5e-16:283:70//AC003658

F-PLACE1006196//Mouse RNA helicase and RNA-dependent ATPase from the DEA  
D box family mRNA, complete cds.//2.2e-94:648:84//L25125

F-PLACE1006205//Human Xp22 cosmid U250A9, complete sequence.//0.15:533:5  
8//U75931

F-PLACE1006223//F24L20-T7 IGF *Arabidopsis thaliana* genomic clone F24L20,  
genomic survey sequence.//0.0068:175:64//B19803

F-PLACE1006225//CIT-HSP-2335I23.TF CIT-HSP *Homo sapiens* genomic clone 23  
35I23, genomic survey sequence.//2.1e-19:149:90//AQ039880

F-PLACE1006236//Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence.//0.51:290:58//U91327

F-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//7.4e-158:452:96//AC004142

F-PLACE1006246//RPCI11-36I23.TK RPCI-11 Homo sapiens genomic clone RPCI-11-36I23, genomic survey sequence.//2.6e-31:176:97//AQ045400

F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.3e-166:791:98//AB014548

F-PLACE1006262//342E3.TVD CIT978SKA1 Homo sapiens genomic clone A-342E03, genomic survey sequence.//1.0:228:63//B16447

F-PLACE1006288//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20N2, WORKING DRAFT SEQUENCE.//6.6e-172:809:99//AL031320

F-PLACE1006318

F-PLACE1006325//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence.//0.079:396:59//AC004454

F-PLACE1006335//Mouse Ig third hypervariable region (HCDR3), nonproductively rearranged alpha-chain gene VHSB32-D-JH2 region.//1.0:90:67//M55721

F-PLACE1006357//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.16:445:56//AC005504

F-PLACE1006360//Plasmodium falciparum MAL3P7, complete sequence.//6.1e-05:625:57//AL034559

F-PLACE1006368//X.laevis mRNA for KLP2 protein.//3.0e-25:376:68//X94082

F-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//2.0e-146:711:97//AC004232

F-PLACE1006382

F-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//5.1e-110:539:97//AF062085

F-PLACE1006412//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete

sequence.//1.3e-23:463:68//AC005029

F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds.//1.3e-109:525:98//AF069735

F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds.//6.9e-23:531:65//AB011129

F-PLACE1006445//HS\_3071\_A1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=21 Row=E, genomic survey sequence.//4.7e-74:392:95//AQ103347

F-PLACE1006469//Rhodobacter capsulatus strain SB1003, partial genome.//1.1e-40:686:65//AF010496

F-PLACE1006470//T.brucei kinetoplast maxicircle variable region DNA.//0.99:250:59//Z15118

F-PLACE1006482//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING DRAFT SEQUENCE.//4.3e-120:328:98//AL021977

F-PLACE1006488//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//6.5e-86:478:91//X53744

F-PLACE1006492

F-PLACE1006506

F-PLACE1006521//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//0.0010:547:58//AC005083

F-PLACE1006531//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-84:625:80//AF005355

F-PLACE1006534//Caenorhabditis elegans cosmid Y40H7A, complete sequence.//0.00031:671:58//AL033510

F-PLACE1006540

F-PLACE1006552//P.falciparum glutamic acid-rich protein gnen, complete cds.//6.0e-10:636:59//J03998

F-PLACE1006598//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//9.8e-25:170:77//AC006044

F-PLACE1006615//*Homo sapiens* eukaryotic translation initiation factor eI F3, p35 subunit mRNA, complete cds.//6.7e-167:781:99//U97670

F-PLACE1006617//*Homo sapiens* Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//0.98:514:59//AC004470

F-PLACE1006626//*H.sapiens* DNA 3' flanking simple sequence region clone w g2c3.//0.00079:206:62//X76589

F-PLACE1006629//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.0012:576:57//AC004015

F-PLACE1006640//*P.falciparum* complete gene map of plastid-like DNA (IR-B).//0.0018:588:59//X95276

F-PLACE1006673//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0028:469:58//AC 004688

F-PLACE1006678//*Mus musculus* UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase-I (b3GT1) gene, complete cds.//0.00011:184:64//AF029790

F-PLACE1006704//*Mus musculus* dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.0013:380:62//U67916

F-PLACE1006731//Human DNA sequence from PAC 408N23 on chromosome 22q13. Contains HIP, HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATE D P48 PROTEIN), ESTs and STS.//1.5e-78:520:86//Z98048

F-PLACE1006754//*Homo sapiens* chromosome 19, cosmid R29124, complete sequence.//1.9e-135:378:99//AC005626

F-PLACE1006760//CIT-HSP-2336013.TR CIT-HSP *Homo sapiens* genomic clone 23 36013, genomic survey sequence.//0.018:147:66//AQ039246

F-PLACE1006779//*Plasmodium falciparum* chromosome 2, section 63 of 73 of the complete sequence.//2.6e-08:823:58//AE001426

F-PLACE1006782//*Homo sapiens* clone NH0005N18, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.043:252:65//AC005487

F-PLACE1006792//HS\_3165\_B1\_H01\_MR CIT Approved Human Genomic Sperm Libra

ry D *Homo sapiens* genomic clone Plate=3165 Col=1 Row=P, genomic survey sequence.//1.4e-11:249:67//AQ149559

F-PLACE1006795//Mouse eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds.//1.3e-12:155:80//M68513

F-PLACE1006800//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-92, complete sequence.//6.7e-05:391:62//AL010272

F-PLACE1006805//*paramecium* species 1,168 mt dna dimer: replication init. region.//9.1e-09:369:62//K00915

F-PLACE1006815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING DRAFT SEQUENCE.//0.89:465:58//AL031033

F-PLACE1006819//*Homo sapiens* clone DJ1163L11, complete sequence.//1.5e-1 21:618:91//AC005230

F-PLACE1006829//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160 nt].//0.011:145:68//S69350

F-PLACE1006860//*Plasmodium falciparum* MAL3P7, complete sequence.//2.2e-0 7:691:58//AL034559

F-PLACE1006867//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 323M4, WORKING DRAFT SEQUENCE.//1.5e-132:643:98//AL033378

F-PLACE1006878

F-PLACE1006883//*Mycobacterium tuberculosis* H37Rv complete genome; segment 138/162.//1.0:236:62//Z95120

F-PLACE1006901//*Mus musculus* t complex testis-specific protein (Tctex2) gene, t haplotype, promoter sequence.//2.7e-19:171:81//U21672

F-PLACE1006904

F-PLACE1006917//*H.sapiens* CpG island DNA genomic Mse1 fragment, clone 79 g10, forward read cpg79g10.ft1a.//1.3e-21:131:98//Z63175

F-PLACE1006932//*Mus musculus* FKBP65 binding protein mRNA, complete cds.//0.99:248:61//L07063

F-PLACE1006935//*Homo sapiens* chromosome 9 duplication of the T cell rece

ptor beta locus and trypsinogen gene families.//0.85:161:63//AF029308  
F-PLACE1006956//*Hylobates lar* involucrin gene, complete cds.//0.077:355:  
61//M35447  
F-PLACE1006958//*Mus musculus* osmotic stress protein 94 (Osp94) mRNA, com  
plete cds.//2.9e-89:483:86//U23921  
F-PLACE1006961//*Saccharomyces cerevisiae* mitochondrial tRNA-Tyr, tRNA-As  
n, & tRNA-Met genes.//1.6e-06:651:58//AJ223323  
F-PLACE1006962//*H.sapiens* irIB mRNA.//7.1e-15:202:71//X63417  
F-PLACE1006966//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*  
● \* from clone Y105E8, WORKING DRAFT SEQUENCE.//1.7e-26:451:61//AL022594  
F-PLACE1006989//cSRL-172A4-u cSRL flow sorted Chromosome 11 specific cos  
mid *Homo sapiens* genomic clone cSRL-172A4, genomic survey sequence.//1.0  
:97:67//B03188  
F-PLACE1007014//*Rattus norvegicus* equilbrative nitrobenzylthioinosine-in  
sensitive nucleoside transporter mRNA, complete cds.//4.2e-07:592:58//AF  
015305  
F-PLACE1007021//*Homo sapiens* chromosome 19, cosmid F16403, complete sequ  
ence.//5.1e-17:285:70//AC005777  
F-PLACE1007045//Human DNA sequence from PAC 181N1 on chromosome X contai  
ns ESTs, STS polymorphic CA repeat\*.//6.2e-131:775:89//Z82899  
F-PLACE1007053//*Homo sapiens* clone DJ0810E06, WORKING DRAFT SEQUENCE, 8  
unordered pieces.//1.7e-143:675:99//AC004895  
F-PLACE1007068//*Homo sapiens* chromosome 17, clone hRPK.214\_0\_1, complete  
sequence.//1.3e-131:652:97//AC005224  
F-PLACE1007097//*Homo sapiens* DNA sequence from BAC 55C20 on chromosome 6  
. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a  
beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE ps  
eudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudo  
gene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences)

and a CA repeat polymorphism, complete sequence.//8.3e-158:768:97//AL02  
1368

F-PLACE1007105//*Mus musculus* *muskelin* mRNA, complete cds.//4.1e-124:687:  
91//U72194

F-PLACE1007111//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC336 genomic  
sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:586:56//  
AC005139

F-PLACE1007112//HS\_2234\_B2\_G10\_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2234 Col=20 Row=N, genomic survey  
sequence.//0.26:200:62//AQ087801

F-PLACE1007132//CIT978SK-A-211C6.TVB CIT978SK *Homo sapiens* genomic clone  
A-211C6, genomic survey sequence.//1.3e-40:255:92//B72112

F-PLACE1007140//QN1 orf [Coturnix coturnix, japonica, K2 neuroretinal ce  
lls, mRNA Partial, 3884 nt].//4.9e-15:386:62//S68151

F-PLACE1007178//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-420 genomic  
sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.011:329:61  
//AC005140

F-PLACE1007226//Human lipocortin (LIP) 2 gene, upstream region.//0.0036:  
180:63//M62899

F-PLACE1007238//FMR1 {CGG repeats} [human, Fragile X syndrome patient, G  
enomic, 429 nt].//2.8e-08:269:63//S74494

F-PLACE1007239//*Homo sapiens* mRNA for transcription elongation factor S-  
II, hS-II-T1, complete cds.//6.3e-57:405:87//D50495

F-PLACE1007242//HS\_3006\_A1\_B11\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3006 Col=21 Row=C, genomic survey  
sequence.//0.088:191:59//AQ089443

F-PLACE1007243//Human transporter protein (g17) mRNA, complete cds.//7.9  
e-12:245:66//U49082

F-PLACE1007257//*Homo sapiens* mRNA for dia-12c protein.//5.2e-144:677:98/

/Y15908

F-PLACE1007274//HS\_3003\_A1\_D08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=G, genomic survey sequence.//7.4e-49:345:85//AQ294154

F-PLACE1007276//Fugu rubripes GSS sequence, clone 014010aG11, genomic survey sequence.//0.0052:228:62//AL024982

F-PLACE1007282//F.rubripes GSS sequence, clone 019007aB3, genomic survey sequence.//0.024:289:58//AL011743

F-PLACE1007286//Human Chromosome 16 BAC clone CIT987SK-A-256A9, complete sequence.//0.0048:185:69//AC002492

F-PLACE1007301//Dictyostelium discoideum gene for TRFA, complete cds.//0.069:761:57//AB009080

F-PLACE1007317

F-PLACE1007342

F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//5.4e-120:567:98//AF096870

F-PLACE1007367//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-59:613:75//AC005077

F-PLACE1007375//Caenorhabditis elegans cosmid D2092.//1.8e-12:193:70//U88167

F-PLACE1007386

F-PLACE1007402//HS\_2170\_A2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2170 Col=24 Row=G, genomic survey sequence.//5.6e-06:162:67//AQ125590

F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 2 mRNA, complete sequence.//1.6e-25:165:93//AF093772

F-PLACE1007416

F-PLACE1007450//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.9e-34:764:62//AC003973

F-PLACE1007452//*Mus musculus* bet3 (Bet3) mRNA, complete cds.//4.1e-17:37  
4:64//AF041433

F-PLACE1007454//*Homo sapiens* (clone s153) mRNA fragment.//8.1e-52:317:93  
//L40391

F-PLACE1007460//Human DNA sequence from clone 914P14 on chromosome Xq23  
Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat,  
GSS, complete sequence.//0.0019:280:64//AL031117

F-PLACE1007478//*Homo sapiens* Chromosome 16 BAC clone CIT987-SKA-345G4  
complete genomic sequence, complete sequence.//2.5e-24:362:71//AC002302

F-PLACE1007484

F-PLACE1007488//*Danio rerio* faciogenital dysplasia protein (fgd) mRNA, c  
omplete cds.//3.8e-14:293:63//AF017370

F-PLACE1007507//Human DNA sequence from clone 105D16 on chromosome Xp11.  
3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat  
, STS, complete sequence.//4.6e-10:152:75//AL031311

F-PLACE1007511//*Homo sapiens* chromosome 17, clone hRPC.1110\_E\_20, comple  
te sequence.//3.6e-139:477:98//AC004231

F-PLACE1007524//*Plasmodium falciparum* microsatellite 14C sequence.//0.00  
55:395:59//AF015461

F-PLACE1007525//*Trypanoplasma borelli* mitochondrion cytochrome oxidase s  
ubunit 1 (cox1), cytochrome oxidase subunit 2 (cox2), and apocytochrome  
b (cytb) genes, complete cds, and complete 9S rRNA gene and partial 12S  
rRNA gene.//0.0013:550:58//U11682

F-PLACE1007537//*H.sapiens* CpG island DNA genomic Mse1 fragment, clone 19  
8g6, reverse read cpg198g6.rt1a.//0.98:121:67//Z60280

F-PLACE1007544//*Mus musculus* chromosome 14 marker um-m24 GA dinucleotide  
DNA sequence.//2.3e-10:141:75//U31508

F-PLACE1007547//*Homo sapiens* mRNA for KIAA0661 protein, complete cds.//3  
.1e-69:733:71//AB014561

F-PLACE1007557//*Drosophila yakuba* mitochondrial DNA molecule.//0.022:393

:61//X03240

F-PLACE1007583//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 545L17, WORKING DRAFT SEQUENCE.//3.6e-114:565:97//AL031665

F-PLACE1007598//CIT-HSP-2371G14.TF CIT-HSP *Homo sapiens* genomic clone 23  
71G14, genomic survey sequence.//2.0e-22:304:70//AQ111183

F-PLACE1007618//*Homo sapiens* chromosome 17, clone hRPK.642\_C\_21, comple  
te sequence.//1.0:386:59//AC005245

F-PLACE1007621

● F-PLACE1007632//*Homo sapiens* 12p13.3 PAC RPCI5-940J5 (Roswell Park Cance  
r Institute Human PAC Library) complete sequence.//1.0e-88:276:96//AC006  
064

F-PLACE1007645//Bovine elastin mRNA, partial cds.//2.1e-07:110:79//M2613

2

F-PLACE1007649

F-PLACE1007677//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 968D22, WORKING DRAFT SEQUENCE.//1.2e-21:567:64//AL023755

F-PLACE1007688//*Pseudorabies* virus immediate-early gene.//2.2e-05:287:66  
//X15120

● F-PLACE1007690//*Caenorhabditis elegans* cosmid R07G3.//0.40:122:70//U2345

2

F-PLACE1007697//*Mus musculus* LIM/homeobox (Lhx3) gene fragment.//0.85:11  
7:71//L40483

F-PLACE1007705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 460J8, WORKING DRAFT SEQUENCE.//0.0035:75:88//AL031662

F-PLACE1007706//*Homo sapiens* metalloprotease 1 (MP1) mRNA, complete cds.  
//1.3e-147:709:97//AF061243

F-PLACE1007725//*Arabidopsis thaliana* genomic DNA, chromosome 5, P1 clone  
: MBB18, complete sequence.//1.0:510:58//AB005231

F-PLACE1007729//Human endogenous retrovirus HML6 proviral clone HML6p, putative leader region, gag, pro and pol pseudogenes.//4.8e-136:516:89//U86698

F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//7.9e-155:728:98//AB014585

F-PLACE1007737//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.8e-22:806:60//AC005484

F-PLACE1007743//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-06:510:56//AC005504

F-PLACE1007746//HS\_2268\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=19 Row=N, genomic survey sequence.//0.10:171:63//AQ124780

F-PLACE1007791//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING DRAFT SEQUENCE.//0.63:241:58//AL031749

F-PLACE1007807//Homo sapiens chromosome 17, clone hRPK.879\_D\_6, complete sequence.//1.0e-120:743:87//AC005273

F-PLACE1007810//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.0e-113:739:86//AC003658

F-PLACE1007829//CIT-HSP-2383J22.TR CIT-HSP Homo sapiens genomic clone 2383J22, genomic survey sequence.//1.0e-47:254:97//AQ196438

F-PLACE1007843//F.rubripes GSS sequence, clone 162K02bC12, genomic survey sequence.//1.6e-10:148:72//AL006903

F-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//3.4e-177:844:98//AP00010

F-PLACE1007852//Mouse perlecan mRNA, complete cds.//8.5e-39:243:90//M77174

F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//3

.9e-189:894:98//AB018309

F-PLACE1007866//CIT-HSP-2353D11.TF.1 CIT-HSP Homo sapiens genomic clone  
2353D11, genomic survey sequence.//0.015:279:61//AQ263271

F-PLACE1007877

F-PLACE1007897

F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0487.//2.3e-154:755:97//AB007956

F-PLACE1007946//Human chromosome Y cosmid 56B5 genomic sequence, WORKING  
DRAFT SEQUENCE.//1.1e-59:310:81//AC003097

● F-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.  
//2.1e-61:522:79//AC006157

F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.  
//2.7e-171:813:98//AF084530

F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)  
mRNA, partial cds.//2.5e-153:730:98//AF079529

F-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA,  
partial cds.//3.4e-32:383:74//U13262

F-PLACE1007990//H.sapiens genomic DNA fragment (clone J31A212R).//6.6e-3  
5:198:96//Z94758

● F-PLACE1008000//Mus musculus veli 3 mRNA, complete cds.//1.5e-118:706:88  
//AF087695

F-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4  
unordered pieces.//6.4e-163:786:98//AC005628

F-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA,  
complete cds.//1.2e-95:625:84//L31840

F-PLACE1008045//Caenorhabditis elegans cosmid F17C8, complete sequence.  
/0.016:165:65//Z35719

F-PLACE1008080//Human DNA sequence from cosmid L118G10, Huntington's Disease  
Region, chromosome 4p16.3.//4.0e-07:251:64//Z68883

F-PLACE1008095//RPCI11-21F19.TP RPCI-11 *Homo sapiens* genomic clone RPCI-11-21F19, genomic survey sequence.//1.5e-30:166:99//B85883

F-PLACE1008111//*Aphidius picipes* NADH dehydrogenase 1 gene, mitochondria 1 gene encoding mitochondrial protein, partial cds.//7.5e-06:414:60//AF069163

F-PLACE1008122//*S.cerevisiae* chromosome XV reading frame ORF YOL125w.//0.046:477:59//Z74867

F-PLACE1008129//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0068:446:57//AC004586

F-PLACE1008132//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING DRAFT SEQUENCE.//3.6e-20:111:93//Z82199

F-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.5e-88:866:73//D14849

F-PLACE1008181//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE.//0.0033:727:56//AL034397

F-PLACE1008198//HS\_3073\_A1\_C06\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3073 Col=11 Row=E, genomic survey sequence.//2.3e-12:94:92//AQ171450

F-PLACE1008201//*Homo sapiens* clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.5e-162:791:97//AC005069

F-PLACE1008209

F-PLACE1008231//Mouse testis-specific protein mRNA, complete cds.//0.65:174:66//M26332

F-PLACE1008244//CIT-HSP-2337B4.TR CIT-HSP *Homo sapiens* genomic clone 2337B4, genomic survey sequence.//6.7e-28:165:95//AQ039317

F-PLACE1008273//*B.primigenius* mRNA for coat protein gamma-cop.//2.8e-71:709:71//X92987

F-PLACE1008275//*D.discoideum* actin A-13 gene, 5' flank.//0.12:131:64//M2

9123

F-PLACE1008280//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome System  
s Human BAC Library) complete sequence.//0.011:96:73//AC005913

F-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA,  
complete cds.//8.2e-86:672:77//AF078779

F-PLACE1008329//HS\_2027\_A1\_C06\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2027 Col=11 Row=E, genomic survey  
sequence.//8.7e-09:116:81//AQ244432

F-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequ  
ence.//2.2e-141:670:98//AC005176

F-PLACE1008331//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 u  
nordered pieces.//2.1e-27:157:78//AC005000

F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//1.  
1e-137:659:98//AB014579

F-PLACE1008368//CIT-HSP-2311C9.TR CIT-HSP Homo sapiens genomic clone 231  
1C9, genomic survey sequence.//7.1e-08:398:60//AQ016352

F-PLACE1008369//HS\_2251\_B1\_A02\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2251 Col=3 Row=B, genomic survey s  
equence.//2.1e-35:217:93//AQ066512

F-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complet  
e sequence.//1.4e-11:403:64//AC005856

F-PLACE1008398//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 215D11, WORKING DRAFT SEQUENCE.//3.7e-144:681:99//AL034417

F-PLACE1008401//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4  
, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered  
pieces.//2.8e-45:257:96//AC004604

F-PLACE1008402//Homo sapiens mRNA for p115, complete cds.//4.3e-148:711:  
98//D86326

F-PLACE1008405//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic

sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.089:672:56//AC004688

F-PLACE1008424

F-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 7/11. //1.0e-88:331:84//AB020864

F-PLACE1008429//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//0.55:530:58//U62317

F-PLACE1008437//CIT-HSP-2376H4.TR CIT-HSP Homo sapiens genomic clone 2376H4, genomic survey sequence.//3.3e-78:349:94//AQ112479

F-PLACE1008455//HS\_2064\_B1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=17 Row=J, genomic survey sequence.//4.7e-59:471:81//AQ246589

F-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//8.9e-43:307:73//AC004526

F-PLACE1008465//CIT-HSP-2163F24.TR CIT-HSP Homo sapiens genomic clone 2163F24, genomic survey sequence.//8.9e-41:210:99//B90014

F-PLACE1008488//Mus musculus mRNA for testis-specific protein kinase 1, complete cds.//0.00013:516:58//AB003494

F-PLACE1008524//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34B21, WORKING DRAFT SEQUENCE.//1.3e-161:778:98//AL031778

F-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//1.1e-78:191:100//AF045555

F-PLACE1008532//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//3.8e-24:257:70//Z93097

F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//1.0e-13:215:71//AC004997

F-PLACE1008568//Human DNA sequence from PAC 388N15 on chromosome Xq21.1. //0.66:263:64//Z99571

F-PLACE1008584//Homo sapiens cosmid clone U39B3 from Xp22.1-22.2, complete sequence.//1.1e-19:315:68//U73023

F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-173:812:98//AB018334

F-PLACE1008621//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.9e-09:198:71//AC005077

F-PLACE1008625//Homo sapiens chromosome 5, PAC clone 45L14 (LBNL H91), complete sequence.//0.68:568:59//AC005373

F-PLACE1008626//HS\_3221\_A2\_F03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=6 Row=K, genomic survey sequence.//1.7e-13:147:82//AQ180967

F-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//9.7e-98:586:88//Y12836

F-PLACE1008629//CIT-HSP-2012I4.TR CIT-HSP Homo sapiens genomic clone 2012I4, genomic survey sequence.//0.00085:203:66//B53732

F-PLACE1008630//Sequence 26 from Patent WO9517522.//9.7e-05:97:80//A45356

F-PLACE1008643//Human mRNA for inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP), complete cds.//1.4e-23:299:64//D38595

F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//1.1e-133:622:99//AF044333

F-PLACE1008693//CIT-HSP-2346F2.TF CIT-HSP Homo sapiens genomic clone 2346F2, genomic survey sequence.//0.24:89:76//AQ060732

F-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//1.4e-94:420:97//AF038406

F-PLACE1008715//CIT-HSP-2294K20.TR CIT-HSP Homo sapiens genomic clone 2294K20, genomic survey sequence.//2.1e-70:349:98//AQ007199

F-PLACE1008748//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequ

ence, complete sequence.//0.14:347:59//AC004260

F-PLACE1008757//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//7.9e-25:244:71//AC003037

F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds .//4.5e-120:503:97//AF060543

F-PLACE1008798//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.00026:370:61//AF001549

F-PLACE1008807//CIT-HSP-2334B19.TF CIT-HSP Homo sapiens genomic clone 23 34B19, genomic survey sequence.//3.3e-08:220:65//AQ036643

F-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//1.7e-120:470:97//AF030933

F-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//2.8e-87:50 4:89//AF032668

F-PLACE1008851//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1 p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//4.0e-21:212:74//AL021920

F-PLACE1008854

F-PLACE1008867//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//4.7e-77:477:84//Z82209

F-PLACE1008887//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//3.4e-53:699:70//AC005539

F-PLACE1008902//Mouse G-alpha-13 protein mRNA, complete cds.//2.1e-06:16 4:68//M63660

F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//6. 4e-158:753:98//AB018308

F-PLACE1008925//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180 G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00013:400:63//AC00204

2

F-PLACE1008934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 1104E15, WORKING DRAFT SEQUENCE.//7.4e-05:145:71//AL022312

F-PLACE1008941//Human zinc finger protein (ZNF141) mRNA, complete cds.//  
4.3e-41:282:87//L15309

F-PLACE1008947//Pseudorabies virus with upstream and downstream sequences  
.//5.9e-15:710:60//M34651

F-PLACE1009020//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//1.9e-21:167:86//AQ253727

F-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23

● Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//4.1e-152:763:97//AL031117

F-PLACE1009039//HS\_2034\_A2\_F08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=16 Row=K, genomic survey sequence.//0.17:252:59//AQ230137

F-PLACE1009045//HS\_3185\_B2\_B03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=6 Row=D, genomic survey sequence.//1.9e-34:260:86//AQ172861

F-PLACE1009048//Pig pituitary glycoprotein hormone alpha subunit gene, 5' flank and exon 1.//4.7e-70:463:80//D00766

● F-PLACE1009050//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.63:280:61//AC004241

F-PLACE1009060//Mus musculus mRNA for Alix (ALG-2-interacting protein X), complete CDS.//5.9e-113:725:85//AJ005073

F-PLACE1009090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1045J21, WORKING DRAFT SEQUENCE.//9.1e-27:222:84//AL021919

F-PLACE1009091//Homo sapiens clone DJ0968I16, complete sequence.//0.027:630:58//AC006016

F-PLACE1009094

F-PLACE1009099//Mouse zinc finger protein (mkr4) mRNA, partial cds.//2.1  
e-85:726:76//M36515

F-PLACE1009110

F-PLACE1009111//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 138B7, WORKING DRAFT SEQUENCE.//6.0e-12:362:64//Z98752

F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3  
(XRCC3) mRNA, complete cds.//3.4e-138:671:97//AF035586

F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds.//3.6e-23:718  
:59//D25215

F-PLACE1009150//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRA  
FT SEQUENCE.//6.1e-142:684:98//AJ011929

F-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/  
28, WORKING DRAFT SEQUENCE.//4.3e-36:227:77//AP000031

F-PLACE1009158//H.sapiens genomic sequence for ERCC2 gene 3' region invol  
ved in DNA excision repair.//1.0:173:60//X52222

F-PLACE1009166

F-PLACE1009172//Human BAC clone 7E17 from 12q, complete sequence.//4.0e-  
35:257:85//AC002070

F-PLACE1009174//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Sys  
tems Human BAC Library) complete sequence.//2.9e-19:288:72//AC004805

F-PLACE1009183//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone  
: MHJ24, complete sequence.//0.053:388:60//AB008266

F-PLACE1009186//Rattus norvegicus fracture callus 1 (FxG1) mRNA, comple  
te cds.//1.8e-50:317:89//AF061242

F-PLACE1009190//RPCI11-81N5.TJ RPCI11 Homo sapiens genomic clone R-81N5,  
genomic survey sequence.//0.91:114:67//AQ281881

F-PLACE1009200//CITBI-E1-2509J16.TF CITBI-E1 Homo sapiens genomic clone  
2509J16, genomic survey sequence.//2.8e-44:175:83//AQ262198

F-PLACE1009230//H.sapiens gene for pregnancy specific beta-1 glycoprotei

n.//1.1e-106:495:88//X63203

F-PLACE1009246//HS\_3058\_B1\_A06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=11 Row=B, genomic survey sequence.//0.10:175:68//AQ185945

F-PLACE1009298//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.8e-94:575:89//U47024

F-PLACE1009308//Human clone mcag32 chromosome 7 CTG repeat region.//0.00 17:350:62//U23862

F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds.//3.0e-06:411:59//U83192

F-PLACE1009328//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191P20, WORKING DRAFT SEQUENCE.//5.7e-138:830:86//AL034399

F-PLACE1009335//Human (lambda) DNA for immunoglobin light chain.//0.071: 253:62//D87015

F-PLACE1009338//RPCI11-74N24.TV RPCI11 Homo sapiens genomic clone R-74N2 4, genomic survey sequence.//2.4e-34:180:100//AQ268811

F-PLACE1009368

F-PLACE1009375

F-PLACE1009388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1014D13, WORKING DRAFT SEQUENCE.//2.0e-37:288:84//AL022311

F-PLACE1009398//Human DNA binding protein (HPF2) mRNA, complete cds.//4. 3e-78:730:74//M27878

F-PLACE1009404//SMD homolog [mice, liver, mRNA Partial, 199 nt].//0.16:9 5:71//S71494

F-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//1.6e-150:701:99//AC005919

F-PLACE1009434//Mus musculus clone OST431, genomic survey sequence.//2.9 e-73:442:88//AF046700

F-PLACE1009443//Mycobacterium tuberculosis H37Rv complete genome; segmen

t 148/162.//0.012:582:56//AL022022

F-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230)  
mRNA, complete cds.//4.6e-21:146:93//AF012872

F-PLACE1009459//Mus musculus clone OST9217, genomic survey sequence.//2.  
9e-31:264:81//AF046660

F-PLACE1009468//Sequence 1 from patent US 5580968.//1.9e-83:567:84//I305  
36

F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, co  
mplete sequence.//1.9e-142:704:97//AC004531

F-PLACE1009477//Human 11p14.3 PAC clone pDJ939m16, complete sequence.//2  
.2e-09:235:68//AC004601

F-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete  
sequence.//2.9e-83:171:92//U91321

F-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22  
q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytoh  
esin-2, Arno, ARF exchange factor) LIKE protein, an unknown gene and a g  
ene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, com  
plete sequence.//3.8e-69:175:92//Z94160

F-PLACE1009539//Mus musculus synaptjanin 2 isoform alpha mRNA, complete  
cds.//7.0e-26:237:78//AF041862

F-PLACE1009542//Human DNA sequence from clone 1039K5 on chromosome 22q12  
.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene  
similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG  
island, complete sequence.//3.1e-10:126:79//AL031587

F-PLACE1009571//RPCI11-60K12.TK RPCI11 Homo sapiens genomic clone R-60K1  
2, genomic survey sequence.//1.4e-05:68:91//AQ195869

F-PLACE1009581

F-PLACE1009595//Homo sapiens chromosome 5, P1 clone 1029A7 (LBNL H15), c  
omplete sequence.//6.6e-19:309:70//AC003959

F-PLACE1009596//Rattus norvegicus platelet-activating factor acetylhydro  
lase beta subunit (PAF-AH beta) gene, complete cds.//9.0e-09:485:59//AF0  
16049

F-PLACE1009607//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 409J21, WORKING DRAFT SEQUENCE.//4.9e-43:714:66//Z83824

F-PLACE1009613//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic  
sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.017:655:57//AC  
004157

F-PLACE1009621

F-PLACE1009622//HS-1016-B2-E08-MF.abi CIT Human Genomic Sperm Library C  
Homo sapiens genomic clone Plate=CT 791 Col=16 Row=J, genomic survey seq  
uence://2.7e-15:100:98//B33248

F-PLACE1009637//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic  
sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.63:130:67//AC0  
05308

F-PLACE1009639//S.pombe chromosome II cosmid c24E9.//0.86:509:58//AL0218  
16

F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1  
.4e-171:816:98//AB011159

F-PLACE1009665//Homo sapiens chromosome 17, clone HCIT462L7, complete se  
quence.//3.4e-67:437:87//AC005177

F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.5e-147:  
701:98//AF062534

F-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//1.5e-9  
8:228:100//AC006011

F-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//  
2.2e-130:736:91//AC000109

F-PLACE1009731//M.musculus mRNA for immunity associated protein 38.//1.1  
e-13:311:64//Y08026

F-PLACE1009763//*Homo sapiens* UBA3 (UBA3) mRNA, complete cds.//4.2e-125:6  
02:98//AF046024

F-PLACE1009794

F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25  
-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3,  
EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein  
Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part o  
f a novel gene similar to hypothetical proteins *S. pombe* C22F3.14C and *C  
elegans* C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1  
.3e-73:271:84//AL030996

F-PLACE1009845

F-PLACE1009861//*B. tauris* cathepsin B mRNA, 3' end.//0.00023:147:65//M646  
20

F-PLACE1009879//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 159A1, WORKING DRAFT SEQUENCE.//4.9e-27:725:63//AL034397

F-PLACE1009886//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 167A19, WORKING DRAFT SEQUENCE.//8.2e-12:135:82//AL031427

F-PLACE1009888//F14G3-T7 IGF *Arabidopsis thaliana* genomic clone F14G3, g  
enomic survey sequence.//0.0044:232:60//AQ251431

F-PLACE1009908//*S. pombe* chromosome I cosmid c3F10.//1.5e-19:559:59//Z693  
69

F-PLACE1009921//*Homo sapiens* cosmid clone HDAB (1S149) insert DNA, compl  
ete cosmid.//5.9e-48:304:87//M63005

F-PLACE1009924//*Homo sapiens* chromosome 16p11.2 BAC clone CIT987SK-20110  
4, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.4e-51:481:78//AC004529

F-PLACE1009925//nbxb0027C22r CUGI Rice BAC Library *Oryza sativa* genomic  
clone nbxb0027C22r, genomic survey sequence.//0.98:220:67//AQ272066

F-PLACE1009935//Sequence 16 from patent US 5552281.//0.030:152:67//I2565

F-PLACE1009947//*Homo sapiens* clone GS096J14, WORKING DRAFT SEQUENCE, 3 u  
nordered pieces.//2.6e-12:322:67//AC006026

F-PLACE1009971

F-PLACE1009992//HS\_3178\_B1\_F04\_T7 CIT Approved Human Genomic Sperm Libra  
ry D *Homo sapiens* genomic clone Plate=3178 Col=7 Row=L, genomic survey s  
equence.//4.9e-23:142:95//AQ150311

F-PLACE1009995//*Caenorhabditis elegans* cosmid C01A2, complete sequence.//  
/0.00019:231:64//Z81029

F-PLACE1009997//*Rattus norvegicus* A-kinase anchoring protein AKAP 220 mRNA  
, complete cds.//7.9e-87:552:80//U48288

F-PLACE1010023

F-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-  
22.3. Contains three novel genes, one similar to *C. elegans* Y63D3A.4 and  
one similar to (predicted) plant, worm, yeast and archaea bacterial gen  
es, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and put  
ative CpG islands, complete sequence.//6.9e-101:181:98//AL031775

F-PLACE1010053//*M. musculus* Spnr mRNA for RNA binding protein.//2.3e-136:  
689:95//X84692

F-PLACE1010069//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 212A2, WORKING DRAFT SEQUENCE.//0.0090:383:60//Z95114

F-PLACE1010074//*Homo sapiens* sorting nexin 2 (SNX2) mRNA, complete cds.//  
/1.8e-166:792:98//AF065482

F-PLACE1010076//Mouse mRNA for TGF-beta type I receptor, complete cds.//  
7.5e-13:203:77//D25540

F-PLACE1010083//*Homo sapiens* mRNA for KIAA0456 protein, partial cds.//3.  
0e-152:727:98//AB007925

F-PLACE1010089//HS\_3111\_A1\_E08\_T7 CIT Approved Human Genomic Sperm Libra  
ry D *Homo sapiens* genomic clone Plate=3111 Col=15 Row=I, genomic survey  
sequence.//4.8e-07:124:78//AQ101268

F-PLACE1010096//*R. norvegicus* mRNA for 100 kDa protein.//1.2e-108:700:85/  
/X64411

F-PLACE1010102//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC357 genomic  
sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-07:476:60//  
AC005506

F-PLACE1010105//*Homo sapiens* actin binding protein MAYVEN mRNA, complete  
cds.//3.8e-25:728:60//AF059569

F-PLACE1010106//Human DNA sequence from PAC 127B14 on chromosome Xq22.//  
6.5e-25:488:63//Z93928

F-PLACE1010134//*S. pombe* chromosome I cosmid c29B12.//1.9e-13:238:67//Z99  
164

F-PLACE1010148//*Homo sapiens* partial human cDNA (660 bp).//4.8e-83:409:9  
8//AJ222636

F-PLACE1010152//CIT-HSP-2381F24.TF CIT-HSP *Homo sapiens* genomic clone 23  
81F24, genomic survey sequence.//1.5e-28:163:98//AQ196757

F-PLACE1010181//*Homo sapiens* PAC clone DJ1139I01 from Xq23, complete seq  
uence.//2.4e-15:197:72//AC004973

F-PLACE1010194//*Ictalurus punctatus* tumor suppressor p53 mRNA, complete c  
ds.//3.0e-14:181:74//AF074967

F-PLACE1010202//*Homo sapiens* mRNA for MBNL protein.//1.2e-27:509:66//Y13  
829

F-PLACE1010231//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 287G14, WORKING DRAFT SEQUENCE.//2.3e-101:194:95//AL033377

F-PLACE1010261//*Homo sapiens* mRNA for KIAA0448 protein, complete cds.//5  
.8e-145:693:97//AB007917

F-PLACE1010270//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC588 genomic  
sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.1e-05:347:60//  
AC004710

F-PLACE1010274//*Caenorhabditis elegans* cosmid C01A2, complete sequence.//

/0.00040:231:64//Z81029

F-PLACE1010293//*Homo sapiens* chromosome 2 PAC RPCI3-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.5e-25:344:70//AC004464

F-PLACE1010310//*Homo sapiens* DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//3.5e-10:185:67//AL031005

F-PLACE1010321//Human DNA sequence from clone 299D3 on chromosome 22q13. 3, complete sequence.//0.010:524:58//Z84468

● F-PLACE1010324//CIT-HSP-2335J21.TR CIT-HSP *Homo sapiens* genomic clone 23 35J21, genomic survey sequence.//9.1e-90:448:97//AQ041837

F-PLACE1010329//*Apis mellifera ligustica* complete mitochondrial genome.//2.8e-08:384:64//L06178

F-PLACE1010341//HS-1047-A2-C04-MR.abi CIT Human Genomic Sperm Library C *Homo sapiens* genomic clone Plate=CT 830 Col=8 Row=E, genomic survey sequence.//4.1e-21:141:92//B38252

F-PLACE1010362//*Mycobacterium tuberculosis* H37Rv complete genome; segment 155/162.//0.94:398:57//AL022121

● F-PLACE1010364//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\* \* from clone Y102G3, WORKING DRAFT SEQUENCE.//0.11:404:56//AL020985

F-PLACE1010383//*Homo sapiens* chromosome 17, clone hCIT.186\_H\_2, complete sequence.//0.066:88:76//AC004675

F-PLACE1010401//CIT-HSP-2367K17.TR CIT-HSP *Homo sapiens* genomic clone 23 67K17, genomic survey sequence.//2.4e-71:454:88//AQ076825

F-PLACE1010481//*Bos taurus* C5-glucuronyl epimerase mRNA, partial cds.//7.5e-134:722:93//AF003927

F-PLACE1010491//*Homo sapiens* Cre binding protein-like 2 mRNA, complete cds.//2.2e-150:702:99//AF039081

F-PLACE1010492

F-PLACE1010522//Homo sapiens cosmid LM1937 from Xq28.//0.022:405:60//U82

695

F-PLACE1010529//Sequence 1 from patent US 5776717.//2.9e-145:684:98//AR0  
16417

F-PLACE1010547//Human DNA sequence from clone 790B6 on chromosome 20p11.  
22-12.2. Contains STSs and GSSs, complete sequence.//1.0:283:61//AL03167  
7

F-PLACE1010562//RPCI11-65I16.TK RPCI11 Homo sapiens genomic clone R-65I1  
6, genomic survey sequence.//0.017:216:67//AQ200831

● F-PLACE1010579//Homo sapiens full length insert cDNA YI23D12.//3.9e-19:1  
47:89//AF075014

F-PLACE1010580//Mouse RNA helicase and RNA-dependent ATPase from the DE  
D box family mRNA, complete cds.//6.4e-96:559:89//L25125

F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14  
p (PEX14) mRNA, complete cds.//3.1e-146:707:97//AF045186

F-PLACE1010616//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic  
sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.045:454:59//AC  
005308

● F-PLACE1010622//Plasmodium falciparum MAL3P2, complete sequence.//9.1e-0  
7:378:60//AL034558

F-PLACE1010624//Streptomyces coelicolor cosmid 5A7.//1.4e-05:518:61//AL0  
31107

F-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21  
unordered pieces.//5.0e-137:675:97//AC004846

F-PLACE1010629//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10,  
complete sequence.//2.5e-17:187:80//AC004682

F-PLACE1010630//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clon  
e: K21P3, complete sequence.//0.21:159:64//AB016872

F-PLACE1010631//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 u

nordered pieces.//1.2e-144:720:97//AC005069

F-PLACE1010661

F-PLACE1010662//Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project).//0.90:257:61//AL021960

F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds.//3.3e-73:697:74//U35376

F-PLACE1010714//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.010:447:59//AC004583

F-PLACE1010720//Mouse TPA-induced TIS11 mRNA.//2.0e-86:535:88//X14678

F-PLACE1010739//HS\_2013\_B2\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=20 Row=D, genomic survey sequence.//5.7e-87:435:97//AQ235864

F-PLACE1010743//R.norvegicus mRNA for myr5.//1.7e-87:582:85//X77609

F-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//4.7e-45:235:99//AC005921

F-PLACE1010771//M.musculus HCNGP mRNA.//1.6e-135:801:88//X68061

F-PLACE1010786//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-15, complete sequence.//0.35:334:60//AL010221

F-PLACE1010800//RPCI11-79H17.TV RPCI11 Homo sapiens genomic clone R-79H17, genomic survey sequence.//5.8e-18:168:82//AQ284252

F-PLACE1010802//Human Chromosome X clone bWXD531, complete sequence.//1.6e-30:693:63//AC004384

F-PLACE1010811//RPCI11-51N5.TK RPCI11 Homo sapiens genomic clone R-51N5, genomic survey sequence.//8.3e-11:142:78//AQ052380

F-PLACE1010833//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467K16, WORKING DRAFT SEQUENCE.//7.3e-40:147:88//AL031283

F-PLACE1010856//M.musculus mRNA for utrophin.//7.3e-17:150:86//Y12229

F-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 11/11

./1.4e-94:422:95//AB020868

F-PLACE1010870//*M.musculus* mRNA for ZT3 zinc finger factor./1.3e-93:530  
:90//Z67747

F-PLACE1010877//*Homo sapiens* mRNA for KIAA0610 protein, partial cds./1.  
1e-147:694:98//AB011182

F-PLACE1010891

F-PLACE1010896//Mouse BAC mbac20 from 14D1-D2 (T-Cell Receptor Alpha Loc  
us), complete sequence./3.9e-26:394:68//AC003997

F-PLACE1010900

● F-PLACE1010916//HS\_2242\_A1\_C04\_MF CIT Approved Human Genomic Sperm Libra  
ry D *Homo sapiens* genomic clone Plate=2242 Col=7 Row=E, genomic survey s  
equence./1.0e-78:391:97//AQ146687

F-PLACE1010917

F-PLACE1010925//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC69 genomic  
sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces./0.11:629:56//AC00  
4688

F-PLACE1010926//*Homo sapiens* mRNA for KIAA0554 protein, partial cds./9.  
5e-138:653:98//AB011126

● F-PLACE1010942//*Homo sapiens* intersectin short form mRNA, complete cds./  
/5.6e-90:437:98//AF064243

F-PLACE1010944//*Homo sapiens* full length insert cDNA clone ZD38E12./1.4  
e-09:208:68//AF086247

F-PLACE1010947

F-PLACE1010954//CIT-HSP-2283D9.TR CIT-HSP *Homo sapiens* genomic clone 228  
3D9, genomic survey sequence./2.1e-29:190:91//B98965

F-PLACE1010960//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from contig 4-52, complete sequence./0.00074:421:60//AL010226

F-PLACE1010965//CIT-HSP-2386K24.TF.1 CIT-HSP *Homo sapiens* genomic clone  
2386K24, genomic survey sequence./1.8e-84:412:99//AQ240696

F-PLACE1011026//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*

from contig 3-20, complete sequence.//0.00037:257:64//AL008972

F-PLACE1011032//*Homo sapiens* chromosome 5, BAC clone 118L13 (LBNL H176),  
complete sequence.//3.8e-06:315:65//AC005348

F-PLACE1011041//Human Fas-ligand associated factor 3 mRNA, partial cds./  
/1.5e-56:286:98//U70669

F-PLACE1011046//Rat phospholipase C-1 mRNA, complete cds.//1.3e-24:278:7  
6//M20636

F-PLACE1011054//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 981L23, WORKING DRAFT SEQUENCE.//3.8e-27:196:84//AL031686

F-PLACE1011056//*Ovis aries* bactinecin 11 (Bac11) gene, exon 4, and compl  
ete cds.//5.4e-06:182:67//U77049

F-PLACE1011057//protein kinase PRK2 [human, DX3 B-cell myeloma cell line  
, mRNA, 3255 nt].//3.2e-31:169:100//S75548

F-PLACE1011090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 998H6, WORKING DRAFT SEQUENCE.//5.1e-80:479:89//AL031687

F-PLACE1011109//*Rattus norvegicus* nuclear-encoded mitochondrial elongati  
on factor G mRNA, complete cds.//2.3e-24:192:84//L14684

F-PLACE1011114//*S.cerevisiae* chromosome XI reading frame ORF YKR024c.//1  
.4e-14:346:60//Z28249

F-PLACE1011133//T7E9-T7.1 TAMU *Arabidopsis thaliana* genomic clone T7E9,  
genomic survey sequence.//0.010:345:60//B19698

F-PLACE1011143//CIT-HSP-2375J10.TR CIT-HSP *Homo sapiens* genomic clone 23  
75J10, genomic survey sequence.//0.00013:95:76//AQ109305

F-PLACE1011160//*Homo sapiens* PAC clone DJ0808A01 from 7q21.1-q31.1, comp  
lete sequence.//3.7e-111:692:87//AC004893

F-PLACE1011165//*H.sapiens* galactokinase (GK2) mRNA, complete cds.//8.4e-  
31:194:92//M84443

F-PLACE1011185//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-A-249B10,

complete sequence.//3.1e-43:447:72//AC002288

F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds.//3.3e-124:584:99//AF038664

F-PLACE1011214//HS\_2046\_A2\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2046 Col=2 Row=C, genomic survey sequence.//2.0e-39:346:81//AQ305965

F-PLACE1011219

F-PLACE1011221//CITBI-E1-2513F18.TR CITBI-E1 Homo sapiens genomic clone 2513F18, genomic survey sequence.//2.4e-20:119:100//AQ279801

F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds.//4.4e-146:675:99//AB011101

F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.7e-42:212:84//AC005014

F-PLACE1011273//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\* \* from clone Y37D8, WORKING DRAFT SEQUENCE.//1.0:214:60//Z92819

F-PLACE1011291//RPCI11-16P9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-16P9, genomic survey sequence.//8.0e-08:66:98//B81770

F-PLACE1011296//Homo sapiens chromosome 16, cosmid clone 443G8 (LANL), complete sequence.//0.027:135:67//AC004647

F-PLACE1011310//H.sapiens CpG island DNA genomic Mse1 fragment, clone 53c10, reverse read cpbg53c10.rt1b.//1.4e-05:57:100//Z61496

F-PLACE1011325//Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds.//0.077:193:60//L02290

F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//3.1e-150:699:99//AF102265

F-PLACE1011340//Homo sapiens chromosome 17, clone hRPK.388\_F\_14, complete sequence.//2.4e-38:186:83//AC005375

F-PLACE1011371//Mus musculus PK-120 precursor (itih-4) mRNA, complete cds.//6.0e-35:689:63//AF023919

F-PLACE1011375//*Mus musculus* Kv3.4 gene, exon 4.//6.0e-88:584:86//AJ0103

10

F-PLACE1011399//*paramecium* species 7,325 mt dna dimer: replication init. region.//0.00011:255:63//K00919

F-PLACE1011419//*Homo sapiens* chromosome 21 PAC LLNLP704G1150Q13.//0.067:337:62//AJ006996

F-PLACE1011433//*Homo sapiens* mRNA for KIAA0530 protein, partial cds.//4.6e-157:743:98//AB011102

F-PLACE1011452//*Homo sapiens* \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.1e-53:557:73//AJ011929

F-PLACE1011465//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//3.5e-71:498:80//AC004605

F-PLACE1011472//*Homo sapiens* mRNA for KIAA0712 protein, complete cds.//4.8e-151:703:99//AB018255

F-PLACE1011477//*Homo sapiens* sorting nexin 2 (SNX2) mRNA, complete cds.//5.2e-145:675:99//AF065482

F-PLACE1011492//*Ray (T.californica)* acetylcholine receptor beta-subunit mRNA.//1.0:448:59//J00964

F-PLACE1011503

F-PLACE1011520//*Homo sapiens* clone DJ1119N05, complete sequence.//3.8e-147:692:99//AC004968

F-PLACE1011563//*R.norvegicus* mRNA for leucocyte common antigen-related protein (3941 bp).//0.00036:296:61//X83546

F-PLACE1011567//*Homo sapiens* PAC clone DJ1164K10 from 7p21-p22, complete sequence.//1.1e-38:315:82//AC004984

F-PLACE1011576//*Homo sapiens* hematopoietic cell derived zinc finger protein mRNA, complete cds.//1.3e-65:268:86//AF054180

F-PLACE1011586//*Homo sapiens* chromosome 17, clone HRPC890E16, complete sequence.//2.0e-82:188:96//AC004477

F-PLACE1011635//*Homo sapiens* chromosome 17, clone hRPK.214\_0\_1, complete sequence.//1.8e-153:752:97//AC005224

F-PLACE1011641//*Homo sapiens* T-cell receptor alpha delta locus from base s 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//4.8e-05:190:67//AE000660

F-PLACE1011643//*Alcaligenes eutrophus* phaP gene.//0.16:466:59//X85729

F-PLACE1011646//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1013A10, WORKING DRAFT SEQUENCE.//9.1e-19:156:76//AL033383

F-PLACE1011649

● F-PLACE1011650//*Homo sapiens* retinol dehydrogenase gene, complete cds.//6.4e-09:172:74//AF037062

F-PLACE1011664//*D. melanogaster* crn mRNA.//1.1e-52:650:68//X58374

F-PLACE1011675//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.11:443:58//AC005507

F-PLACE1011682//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//0.31:127:71//AL008719

● F-PLACE1011719//Human BAC clone RG369K23 from 7q31, complete sequence.//4.6e-52:461:77//AC002487

F-PLACE1011725

F-PLACE1011729//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:320:62//AC004737

F-PLACE1011749//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00031:544:59//AC004157

F-PLACE1011762//*Homo sapiens* BAC clone RG437L15 from 8q21, complete sequence.//2.4e-115:682:90//AC004003

F-PLACE1011778//RPCI11-22D17.TVB RPCI-11 *Homo sapiens* genomic clone RPCI-11-22D17, genomic survey sequence.//2.7e-114:611:93//AQ008944

F-PLACE1011783//CIT-HSP-2317N1.TF CIT-HSP *Homo sapiens* genomic clone 2317N1, genomic survey sequence.//2.3e-17:120:94//AQ042330

F-PLACE1011858//*Gallus domesticus* filamin mRNA, complete cds.//4.1e-24:565:64//U00147

F-PLACE1011874//*Homo Sapiens* Chromosome X clone bWXD312, complete sequence.//2.5e-141:678:98//AC004478

F-PLACE1011875//*Homo sapiens* mRNA for KIAA0580 protein, partial cds.//1.6e-108:526:98//AB011152

F-PLACE1011891//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 439F8, WORKING DRAFT SEQUENCE.//0.0014:330:62//AL021392

F-PLACE1011896//*Mus musculus* Wnt10a mRNA, complete cds.//1.4e-89:678:82//U61969

F-PLACE1011922//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.069:246:61//U81400

F-PLACE1011923//*Homo sapiens* serum-inducible kinase mRNA, complete cds.//1.2e-138:664:98//AF059617

F-PLACE1011962//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//2.4e-07:154:74//AQ175369

F-PLACE1011964//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 322P7, WORKING DRAFT SEQUENCE.//3.7e-22:369:69//AL023799

F-PLACE1011982//HS-1041-A1-B01-MR.abi CIT Human Genomic Sperm Library C *Homo sapiens* genomic clone Plate=CT 823 Col=1 Row=C, genomic survey sequence.//0.44:309:58//B36529

F-PLACE1011995//*Homo sapiens* Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//8.8e-53:687:71//AC00605

F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.

2e-146:690:98//AB018256

F-PLACE2000003//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//1.7e-62:293:88//AC005837

F-PLACE2000006//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//1.4e-116:261:91//AC006057

F-PLACE2000007

F-PLACE2000011//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//5.2e-102:489:99//AC005578

F-PLACE2000014//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING DRAFT SEQUENCE.//0.0095:307:62//AL022574

F-PLACE2000015//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.0e-36:316:81//AC005069

F-PLACE2000017//HS\_3042\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=15 Row=K, genomic survey sequence.//1.0:184:61//AQ098074

F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//4.6e-84:844:72//AF082556

F-PLACE2000030//Human Chromosome 11 Cosmid cSRL16b6, complete sequence.//2.3e-22:233:77//U73638

F-PLACE2000033//C.capitata mRNA for chorion protein s18.//0.0019:342:62//Y08913

F-PLACE2000034//Rattus norvegicus transmembrane receptor Robo1 mRNA, complete cds.//2.8e-13:335:63//AF041082

F-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//7.7e-84:489:90//L08505

F-PLACE2000047//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.0e-28:327:76//U95626

F-PLACE2000050//*Homo sapiens* chromosome 17, clone HRPC41C23, complete sequence.//1.1e-32:527:68//AC003101

F-PLACE2000061//CIT-HSP-2346L20.TF CIT-HSP *Homo sapiens* genomic clone 23 46L20, genomic survey sequence.//1.1e-05:89:83//AQ059010

F-PLACE2000062//Human membrane-associated lectin type-C mRNA.//9.0e-113:662:86//M98457

F-PLACE2000072//*Homo sapiens* ZNF202 beta (ZNF202) mRNA, complete cds.//2.2e-133:631:98//AF027219

F-PLACE2000097//*Homo sapiens* chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-16:119:93//AC005910

F-PLACE2000100//HS\_3184\_A1\_D06\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3184 Col=11 Row=G, genomic survey sequence.//1.5e-80:409:97//AQ150004

F-PLACE2000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//1.0e-172:830:98//AL031848

F-PLACE2000111//*Homo sapiens* DNA, trinucleotide repeats region.//1.0:200:64//AB018491

F-PLACE2000115

F-PLACE2000124//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//6.2e-43:362:80//AC004531

F-PLACE2000132//RPCI11-79F15.TV RPCI11 *Homo sapiens* genomic clone R-79F15, genomic survey sequence.//5.4e-35:206:94//AQ284166

F-PLACE2000136//Human BAC clone 7E17 from 12q, complete sequence.//2.7e-12:814:59//AC002070

F-PLACE2000140//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//3.6e-165:799:97//AL020995

F-PLACE2000164//Canine histamine H2 receptor gene, complete cds.//0.10:392:56//M32701

F-PLACE2000170

F-PLACE2000172//Homo sapiens PAC clone DJ0811017 from 7q21-22, complete sequence.//3.9e-91:552:88//AC006005

F-PLACE2000176//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCR L2-GGT Region, complete sequence.//0.98:201:64//AC004032

F-PLACE2000187

F-PLACE2000216

F-PLACE2000223//RPCI11-12L17.TP RPCI-11 Homo sapiens genomic clone RPCI-11-12L17, genomic survey sequence.//0.00039:325:58//B75888

F-PLACE2000235//Human Chromosome 16 BAC clone CIT987SK-254P9, complete sequence.//7.5e-55:237:78//AC003003

F-PLACE2000246//Homo sapiens chromosome 3p clone RPCI4-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces.//2.4e-92:236:94//AC005902

F-PLACE2000264//Human DNA sequence from clone 391022 on chromosome 6p21. 2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//1.4e-32:331:78//AL031577

F-PLACE2000274//Anthocidaris crassispina mRNA for B2HC, partial cds.//8.5e-48:765:66//AB012308

F-PLACE2000302//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//8.3e-08:662:58//U52064

F-PLACE2000305//Homo sapiens clone DJ1129L24, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.4e-08:95:81//AC006021

F-PLACE2000317//HS\_3183\_B2\_F05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3183 Col=10 Row=L, genomic survey sequence.//2.5e-71:346:99//AQ172747

F-PLACE2000335//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.7e-14:402:65//AC004952

F-PLACE2000341//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.//4.5e-77:555:82//AF026554

F-PLACE2000342//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 ge

nes, complete cds, UL8 gene, partial cds.//1.8e-14:259:71//U66829  
F-PLACE2000347//Human DNA from overlapping chromosome 19-specific cosmid  
s R32543, , and F15613 containing ZNF gene family member, genomic sequen  
ce, complete sequence.//6.0e-34:376:74//AC003006  
F-PLACE2000359//RPCI11-23J20.TKBR RPCI-11 Homo sapiens genomic clone RPC  
I-11-23J20, genomic survey sequence.//8.4e-21:288:69//AQ013849  
F-PLACE2000366//Human Tigger1 transposable element, complete consensus s  
equence.//5.0e-114:692:80//U49973  
F-PLACE2000371//Homo sapiens 12p13.3 PAC RPCI1-29K11 (Roswell Park Cance  
r Institute Human PAC Library) complete sequence.//0.38:356:58//AC005182  
F-PLACE2000373//RPCI11-49C18.TJ RPCI11 Homo sapiens genomic clone R-49C1  
8, genomic survey sequence.//0.064:132:68//AQ051776  
F-PLACE2000379//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BA  
C library) complete sequence.//1.6e-130:776:88//AC003658  
F-PLACE2000394//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Pa  
rk Cancer Institute Human BAC Library) complete sequence.//5.4e-113:808:  
83//AC005909  
F-PLACE2000398//Mouse hexamer repeat sequence (117) homologous to Drosop  
hila 'period' gene.//0.87:286:63//X06967  
F-PLACE2000399  
F-PLACE2000404//Caenorhabditis elegans cosmid R74, complete sequence.//2  
.9e-59:532:68//Z36238  
F-PLACE2000411//Acanthamoeba castellanii transformation-sensitive protei  
n homolog mRNA, complete cds.//0.44:553:56//U89984  
F-PLACE2000419//Human adenosine deaminase (ADA) gene, complete cds.//1.4  
e-56:303:86//M13792  
F-PLACE2000425//HS\_3047\_A1\_H05\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3047 Col=9 Row=0, genomic survey s  
equence.//2.8e-42:224:97//AQ126949

F-PLACE2000427

F-PLACE2000433//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//1.1e-19:363:67//AC005821

F-PLACE2000435//HS\_3036\_B1\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=L, genomic survey sequence.//3.1e-06:184:66//AQ096999

F-PLACE2000438//Caenorhabditis elegans cosmid Y45F10D, complete sequence .//4.6e-23:550:62//AL021492

F-PLACE2000450//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//1.0e-78:604:80//AC006025

F-PLACE2000455//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//8.2e-05:330:63//AC002300

F-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.7e-168:816:97//AC005740

F-PLACE2000465//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSR L140b8, complete sequence.//4.3e-33:296:79//AC002037

F-PLACE2000477//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//3.4e-59:598:74//AC005057

F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds.//7.6e-49:361:84//U81602

F-PLACE3000009//Human placenta (Diff48) mRNA, complete cds.//3.0e-58:713:69//U49187

F-PLACE3000020//R.norvegicus type III adenylyl cyclase mRNA, complete cds.//6.1e-103:600:89//M55075

F-PLACE3000029

F-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//4.4e-115:718:86//Y17267

F-PLACE3000070//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.8e-17:250:74//AC005368

F-PLACE3000103//*Caenorhabditis elegans* cosmid C13F10.//4.6e-07:408:61//U

97006

F-PLACE3000119//\*\*\* SEQUENCING IN PROGRESS \*\*\* *Homo sapiens* chromosome 4  
, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered  
pieces.//1.5e-58:291:86//AC004670

F-PLACE3000121//*Rattus norvegicus* rsec15 mRNA, complete cds.//8.1e-81:83  
7:71//AF032668

F-PLACE3000124//*Homo sapiens* chromosome 17, clone hRPK.85\_B\_7, complete  
sequence.//1.8e-48:330:79//AC005695

F-PLACE3000136

F-PLACE3000142//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 349A12, WORKING DRAFT SEQUENCE.//0.011:294:62//AL033520

F-PLACE3000145//*Gallus gallus* tensin mRNA, 3' end.//6.9e-52:659:68//L066  
62

F-PLACE3000147//Human DNA sequence from clone 267M20 on chromosome Xq22.  
2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs an  
d GSSs, complete sequence.//5.1e-37:305:81//AL031053

F-PLACE3000148//*Homo sapiens* chromosome Y, clone 475I1, complete sequenc  
e.//4.7e-32:766:63//AC004474

F-PLACE3000155//*Homo sapiens* chromosome 17, clone hRPK.597\_M\_12, complet  
e sequence.//7.4e-173:822:98//AC005277

F-PLACE3000156//*Homo sapiens* chromosome 19, overlapping cosmids F18547,  
F11133, R27945, R28830 and R32804, complete sequence.//2.2e-81:783:74//A  
C003682

F-PLACE3000157

F-PLACE3000158//, complete sequence.//1.0e-180:845:97//AC005500

F-PLACE3000160//CIT978SK-152K7.TV CIT978SK *Homo sapiens* genomic clone 15  
2K7, genomic survey sequence.//0.080:259:59//B50878

F-PLACE3000169//*Homo sapiens* chromosome 19, BAC CIT-B-191n6, complete se

quence.//9.8e-158:749:98//AC006130

F-PLACE3000194

F-PLACE3000197//*F.rubripes* GSS sequence, clone 075N04bB7, genomic survey sequence.//1.4e-08:164:68//AL003352

F-PLACE3000199//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//0.0019:277:58//Z82207

F-PLACE3000207//*Homo sapiens* BAC clone GS165L15 from 7p15, complete sequence.//6.6e-21:312:67//AC005013

F-PLACE3000208//*Homo sapiens* (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII intergenic region and (COL7A1) gene, complete cds .//1.0:279:61//L23982

F-PLACE3000218//*Homo sapiens*, WORKING DRAFT SEQUENCE, 52 unordered pieces.//9.3e-43:383:79//AC004086

F-PLACE3000220//RPCI11-54B4.TV RPCI11 *Homo sapiens* genomic clone R-54B4, genomic survey sequence.//2.4e-36:381:76//AQ082056

F-PLACE3000221//*Homo sapiens* clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.2e-135:721:91//AC005231

F-PLACE3000226

F-PLACE3000230//*Homo sapiens* ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//3.3e-80:498:78//U95626

F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.6e-54:254:92//Z98046

F-PLACE3000244//*M.musculus* mRNA for 200 kD protein.//1.4e-139:850:86//X80169

F-PLACE3000254//*Ateline herpesvirus 3 complete genome.*//1.3e-10:399:61//

AF083424

F-PLACE3000271//*Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.*//1.8e-21:350:68//AF001548

F-PLACE3000276//*HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.*//5.7e-45:376:81//AQ231147

F-PLACE3000304//*Homo sapiens chromosome 19, cosmid R26660, complete sequence.*//1.6e-138:650:99//AC005328

● F-PLACE3000310

F-PLACE3000320//*Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.*//1.9e-41:379:77//AL034379

F-PLACE3000322//*Homo sapiens chromosome 17, clone hRPK.209\_J\_20, complete sequence.*//3.3e-35:419:68//AC005822

F-PLACE3000331//*CIT-HSP-2347D24.TR CIT-HSP Homo sapiens genomic clone 23 47D24, genomic survey sequence.*//2.7e-20:119:99//AQ061543

F-PLACE3000339//*Rhodobacter sphaeroides magnesium chelatase subunits Bch I (bchI) and BchD (bchD) genes, complete cds; and BchO (bchO) gene, partial cds.*//0.99:310:58//AF017642

● F-PLACE3000341//*Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.*//7.5e-159:752:98//AC006055

F-PLACE3000350//*Rattus norvegicus serine/threonine protein kinase TA01 mRNA, complete cds.*//2.3e-107:592:92//AF084205

F-PLACE3000352//*Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.*//2.1e-37:480:70//Z83732

F-PLACE3000353

F-PLACE3000362//*Homo sapiens chromosome 17, clone hRPK.215\_P\_18, complete sequence.*//0.00011:373:60//AC005969

F-PLACE3000363

F-PLACE3000365//Human DNA sequence from PAC 227P17, between markers DXS791 and DXS8038 on chromosome X contains CpG island, EST.//0.074:279:61//Z81007

F-PLACE3000373//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-118:653:92//Z92545

F-PLACE3000388//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//2.2e-25:288:71//AC005154

F-PLACE3000399//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//2.3e-69:303:86//Z97630

F-PLACE3000400//Caenorhabditis elegans cosmid H03A11, complete sequence.//0.0063:435:58//Z93239

F-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.8e-25:292:73//AC006023

F-PLACE3000402//RPCI11-20D6.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-20D6, genomic survey sequence.//1.1e-10:154:74//AQ008761

F-PLACE3000405//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//2.9e-41:515:72//AC005701

F-PLACE3000406//cSRL-179E11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-179E11, genomic survey sequence.//2.8e-91:540:89//B03443

F-PLACE3000413

F-PLACE3000416//F19L8-Sp6 IGF Arabidopsis thaliana genomic clone F19L8, genomic survey sequence.//0.0018:664:55//B11305

F-PLACE3000425//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence.//1.1e-16:284:70//AL022719

F-PLACE3000455//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 469D22, WORKING DRAFT SEQUENCE.//3.6e-146:732:96//AL031284

F-PLACE3000475//HS\_2164\_A2\_H10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2164 Col=20 Row=0, genomic survey sequence.//1.5e-07:159:71//AQ132983

F-PLACE3000477//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STS.//2.9e-11:213:70//Z83843

F-PLACE4000009//Sequence 93 from patent US 5616500.//9.9e-08:692:60//I39 845

F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//1. 1e-116:331:100//AB018352

F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.//5.0e-05:244:63//AC004131

F-PLACE4000049//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence.//1.2e-37:385:74//AC005926

F-PLACE4000052//M. musculus abc1 mRNA.//1.5e-110:671:88//X75926

F-PLACE4000063

F-PLACE4000089//M. musculus BOX DNA for regulatory element and promoter region related to EC cell differentiation.//3.7e-12:114:85//X74311

F-PLACE4000093//CIT-HSP-2380K5.TF CIT-HSP Homo sapiens genomic clone 238 0K5, genomic survey sequence.//0.11:245:60//AQ108342

F-PLACE4000100//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//2.9e-19:384:65//AL031848

F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds.//1. 2e-145:684:99//AB007931

F-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//3.7e-62:541:78//AF091234

F-PLACE4000129

F-PLACE4000131//HS\_3139\_B2\_F12\_T7 CIT Approved Human Genomic Sperm Library

ry D *Homo sapiens* genomic clone Plate=3139 Col=24 Row=L, genomic survey sequence.//2.3e-14:221:70//AQ183207

F-PLACE4000147//Human DNA sequence from clone 740A11 on chromosome Xq22.

2-23. Contains part of the COL4A5 gene for Collagen Alpha 5(IV) Chain Precursor. Contains GSSs, complete sequence.//0.28:412:58//AL031622

F-PLACE4000156//Human zinc finger protein ZNF136.//7.2e-88:764:76//U0936

7

F-PLACE4000192

F-PLACE4000211

● F-PLACE4000222//344J1.TVB CIT978SKA1 *Homo sapiens* genomic clone A-344J01, genomic survey sequence.//1.2e-14:177:76//B17158

F-PLACE4000230//*Mus musculus* semaphorin VIA mRNA, complete cds.//9.8e-11 6:662:89//AF030430

F-PLACE4000233//*Homo sapiens* DNA from chromosome 19, BAC 33152, complete sequence.//5.2e-54:363:70//AC003973

F-PLACE4000247

F-PLACE4000250//*Homo sapiens* Xp22-132-134 BAC GSHB-590J15 (Genome System's Human BAC library) complete sequence.//0.0053:229:65//AC004673

● F-PLACE4000252

F-PLACE4000259//*H.sapiens* gene for U5 snRNP-specific 200kD protein.//2.0 e-25:191:87//Z70200

F-PLACE4000261//*Mus musculus* bromodomain-containing protein BP75 mRNA, complete cds.//2.6e-23:314:71//AF084259

F-PLACE4000269//*Rattus norvegicus* rexo70 mRNA, complete cds.//5.5e-122:7 34:88//AF032667

F-PLACE4000270

F-PLACE4000300

F-PLACE4000320//Human FKBP-rapamycin associated protein (FRAP) mRNA, complete cds.//1.4e-21:135:96//L34075

F-PLACE4000323//HS\_2165\_B1\_B02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2165 Col=3 Row=D, genomic survey sequence.//4.3e-08:170:71//AQ125036

F-PLACE4000326//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.//2.8e-06:311:63//M10296

F-PLACE4000344//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.014:252:60//AE001401

F-PLACE4000367

F-PLACE4000369

F-PLACE4000379//CIT-HSP-2350B9.TF CIT-HSP Homo sapiens genomic clone 235 0B9, genomic survey sequence.//9.2e-46:282:86//AQ062661

F-PLACE4000387//CIT-HSP-2382F11.TR CIT-HSP Homo sapiens genomic clone 23 82F11, genomic survey sequence.//0.96:102:70//AQ080649

F-PLACE4000392//Rattus norvegicus polymorphic marker D20UIA1 sequence.//1.2e-05:222:68//AF054088

F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds.//9.6e-46:605:71//AB014540

F-PLACE4000411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//3.2e-29:179:79//AL031984

F-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//4.0e-44:263:92//Z70200

F-PLACE4000445//HS-1053-B1-D02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775 Col=3 Row=H, genomic survey sequence.//0.070:47:100//B41346

F-PLACE4000450

F-PLACE4000465//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//2.3e-07:273:65//AC005065

F-PLACE4000487//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//4.1e-34:351:70//AC005821

F-PLACE4000489//HS\_3012\_B1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3012 Col=9 Row=N, genomic survey sequence.//2.0e-36:220:92//AQ095537

F-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.3e-57:395:79//AC05865

F-PLACE4000521//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.6e-163:770:98//AJ011929

F-PLACE4000522//Feline leukemia virus Notch2 gene, clone FeLV/Notch2-C, partial cds.//4.0e-124:686:90//U47645

F-PLACE4000548

F-PLACE4000558//Bothrops atrox batroxobin gene (EC 3.4.21.29).//0.049:43 5:59//X12747

F-PLACE4000581

F-PLACE4000590//Homo sapiens chromosome Y, clone 475I1, complete sequence.//3.6e-20:747:59//AC004474

F-PLACE4000593//Caenorhabditis elegans cosmid F25D7, complete sequence.//5.6e-16:326:65//Z78418

F-PLACE4000612//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.7e-163:785:97//AC005281

F-PLACE4000638//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.7e-74:707:74//AC006039

F-PLACE4000650

F-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-145:840:89//Y17267

F-PLACE4000670//Sequence 13 from patent US 5712381.//1.0:311:59//I82816

F-SKNMC1000011//Gallus gallus bone sialoprotein II mRNA, complete cds.//0.014:92:73//U10577

F-SKNMC1000013//Orang-utan involucrin gene, complete cds.//0.021:417:59/

/M25312

F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.

6e-147:706:98//AB014554

F-SKNMC1000050//Sequence 5 from patent US 5789181.//1.6e-52:330:90//AR02  
0616

F-SKNMC1000091//Human NK homeobox protein (Nkx6.1) gene, exon 1.//0.0018  
:375:60//U66797

F-THYR01000017//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA,  
complete cds.//6.6e-97:542:84//U91561

● F-THYR01000026//Human DNA sequence from clone 833B7 on chromosome 22q12.  
3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common  
beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS, complete  
sequence.//3.5e-46:353:82//AL008637

F-THYR01000034//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
90L6, WORKING DRAFT SEQUENCE.//0.83:227:61//Z97353

F-THYR01000035//Human Chromosome X clone bWXD187, complete sequence.//1.  
2e-39:303:83//AC004383

F-THYR01000040

● F-THYR01000070//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q  
25.1, complete sequence.//1.3e-05:613:58//AC005383

F-THYR01000072//Homo sapiens mRNA for KIAA0657 protein, partial cds.//2.  
7e-84:722:77//AB014557

F-THYR01000085

F-THYR01000092//CIT-HSP-2013L16.TFB CIT-HSP Homo sapiens genomic clone 2  
013L16, genomic survey sequence.//0.31:186:61//B60606

F-THYR01000107

F-THYR01000111//Human genomic DNA sequence from clone 30801 on chromosome  
Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//6.4e-110:  
690:87//Z93403

F-THYRO1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//1.4e-127:816:85//U49055

F-THYRO1000124//H.sapiens CpG island DNA genomic Mse1 fragment, clone 72 a7, forward read cpg72a7.ft1a.//9.5e-26:169:94//Z62724

F-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//8.5e-154:732:98//AF087142

F-THYRO1000132//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//3.7e-39:315:82//AC002096

F-THYRO1000156//Human DNA sequence from clone 113J7 on chromosome Xp11.2 2-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.2e-21:335:71//AL023574

F-THYRO1000163//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-A-218C7, complete sequence.//8.4e-52:301:88//AC002331

F-THYRO1000173//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//4.0e-89:821:74//M62419

F-THYRO1000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//7.2e-39:293:85//Z82207

F-THYRO1000187//Clostridium tetani gene for tetanus toxin.//0.041:473:57 //X06214

F-THYRO1000190//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//0.38:184:64//AC005746

F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//7.5e-174:805:99//AJ005698

F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.2e-86:616:84//AB014552

F-THYRO1000206//HS\_3047\_A1\_A05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.51:331:63//AQ099134

F-THYRO1000221//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic

'sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.092:738:56//AC  
004157

F-THYR01000241//Gallus gallus genome fragment with pentamer tandem repeats.//0.43:191:62//X00186

F-THYR01000242//Human zinc finger gene HZF7.//2.8e-43:534:64//X60156

F-THYR01000253//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.95:139:68//AC006055

F-THYR01000270

● F-THYR01000279//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//1.4e-174:826:98//AL031664

F-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//3.9e-179:848:98//AB016068

F-THYR01000320//Mus musculus sphingosine-1-phosphate lyase mRNA, complete cds.//1.0e-44:331:83//AF036894

F-THYR01000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//5.7e-112:641:91//L35233

F-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//2.2e-162:763:98//AB018333

● F-THYR01000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//2.2e-32:177:84//U29091

F-THYR01000368//Caenorhabditis elegans cosmid W09G3, complete sequence.//0.97:206:60//Z82080

F-THYR01000381//Arthrobacter sp. glcI gene for beta-1,3-glucanase, complete cds.//0.27:427:62//D23668

F-THYR01000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//9.7e-147:698:98//AC006019

F-THYR01000394//HS\_2061\_A2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2061 Col=8 Row=E, genomic survey s

quence.//1.6e-29:202:91//AQ247672

F-THYR01000395//*Drosophila melanogaster* ring canel protein and ORF2 mRNA  
, complete cds.//4.3e-15:512:59//L08483

F-THYR01000401

3.2e-116:504:80//AF051908

F-THYR01000438//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC492 genomic  
sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-09:539:59//  
AC005308

F-THYR01000452//RPCI11-1C19.TVB RPCI-11 *Homo sapiens* genomic clone RPCI-  
11-1C19, genomic survey sequence.//0.27:132:64//B49573

F-THYR01000471//*Homo sapiens* PAC clone DJ1136G13 from 7q35-q36, complete  
sequence.//1.3e-38:332:81//AC005229

F-THYR01000484//*Homo sapiens* BAC378, complete sequence.//2.2e-37:254:76//  
/U85196

F-THYR01000488//*Homo sapiens* chromosome 5p, BAC clone 50g21 (LBNL H154),  
complete sequence.//6.3e-130:327:97//AC005740

F-THYR01000501//*H.sapiens* Staf50 mRNA.//9.8e-74:615:77//X82200

F-THYR01000502//Human DNA sequence from PAC 436M11 on chromosome Xp22.11  
-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and  
the first coding exon of the RS1 gene for retinoschisis (X-linked, juve  
nile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//0.0  
76:380:59//Z94056

F-THYR01000505

F-THYR01000558//Human PAC clone 127H14 from 12q, complete sequence.//2.4  
e-27:412:69//AC002563

F-THYR01000569//HS\_2178\_B2\_E03\_T7 CIT Approved Human Genomic Sperm Libra  
ry D *Homo sapiens* genomic clone Plate=2178 Col=6 Row=J, genomic survey s  
equence.//1.9e-27:326:74//AQ307499

F-THYR01000570

F-THYR01000585//Homo sapiens protein associated with Myc mRNA, complete cds.//7.4e-167:808:97//AF075587

F-THYR01000596//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//0.99:280:61//U91323

F-THYR01000602//HS\_3037\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=8 Row=J, genomic survey sequence.//1.2e-05:109:75//AQ097057

F-THYR01000605//Homo sapiens map 2p11.2; 83cM from GATA85A06 repeat region, complete sequence.//1.0:84:70//AF067777

● F-THYR01000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//3.4e-174:820:98//AC005546

F-THYR01000637//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//3.6e-38:289:84//AL024474

F-THYR01000641//Plasmodium falciparum MAL3P7, complete sequence.//6.8e-07:540:56//AL034559

F-THYR01000658//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//1.1e-68:468:84//AC005696

● F-THYR01000662//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0072:141:70//AB016874

F-THYR01000666//Mus musculus mRNA for motor domain of KIF9, partial cds.//4.7e-58:367:87//AB001437

F-THYR01000676//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//1.2e-36:396:71//AC005778

F-THYR01000684//Fugu rubripes cosmid 165K09 DNA for GRM7, TRIP, Sand, PRGFR3 genes.//6.6e-13:236:69//AJ010317

F-THYR01000699//RPCI11-50D4.TK RPCI11 Homo sapiens genomic clone R-50D4, genomic survey sequence.//2.7e-09:135:78//AQ052641

F-THYR01000712//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence

ence.//5.2e-17:290:67//AC005053

F-THYRO1000715//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.6e-08:517:60//L14320

F-THYRO1000734//HS\_3233\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=7 Row=D, genomic survey sequence.//6.0e-72:463:89//AQ182143

F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds.//9.7e-34:339:74//AB007871

F-THYRO1000756//M.musculus mRNA for Gal beta1, 3GalNAc alpha2,3-sialyltransferase.//0.00034:349:60//X73523

F-THYRO1000777//S.griseus str0 gene and sts gene cluster.//8.2e-05:625:59//Y08763

F-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//4.0e-70:860:69//U37373

F-THYRO1000787//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 366D1, WORKING DRAFT SEQUENCE.//5.3e-09:221:66//Z97986

F-THYRO1000793

F-THYRO1000796//Cristatella mucedo clone 5.9 microsatellite sequence.//0.34:173:63//AF085422

F-THYRO1000805//Homo sapiens Xp21 PAC RPCI1-37A12 containing exons 10 to 16 of the Duchenne Muscular Dystrophy gene, complete sequence.//7.8e-43:677:66//AC004468

F-THYRO1000815//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//5.5e-43:405:77//AC005914

F-THYRO1000829//CIT-HSP-2387C10.TF.1 CIT-HSP Homo sapiens genomic clone 2387C10, genomic survey sequence.//2.0e-20:159:88//AQ240053

F-THYRO1000843

F-THYRO1000852//Homo sapiens chromosome 19, cosmid R31855, complete sequence.//1.8e-33:445:72//AC005782

F-THYR01000855//*Mus musculus* potassium channel alpha subunit (Kv9.1) mRNA, complete cds.//0.038:208:64//AF008573

F-THYR01000865//*Homo sapiens* PAC clone DJ0283M22 from 14, complete sequence.//1.9e-30:286:74//AC005477

F-THYR01000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 385E7, WORKING DRAFT SEQUENCE.//2.8e-18:186:80//AL031720

F-THYR01000916//*Homo sapiens* clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-78:432:93//AC006015

F-THYR01000926//*Homo sapiens* cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.2e-178:839:98//AF079529

F-THYR01000934//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//3.5e-32:759:63//M77836

F-THYR01000951//*Homo sapiens* Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//4.9e-76:224:93//AC004229

F-THYR01000952

F-THYR01000974//HS\_3238\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3238 Col=2 Row=L, genomic survey sequence.//2.4e-26:154:96//AQ219846

F-THYR01000975//*Plasmodium falciparum* TopoII gene.//0.32:491:58//X79345

F-THYR01000983//Mwgf9A3 exon amplification products from BACs in Mwgf region *Mus musculus* genomic, genomic survey sequence.//7.0e-16:112:94//AQ010457

F-THYR01000984//CIT-HSP-2167017.TR CIT-HSP *Homo sapiens* genomic clone 2167017, genomic survey sequence.//0.00015:186:66//B91313

F-THYR01000988//Human Chromosome 11q12.2 PAC clone pDJ756b9 containing human ferritin heavy chain mRNA (FTH), WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.024:267:63//AC004588

F-THYR01001003

F-THYR01001031//*Homo sapiens* chromosome 17, clone hRPC.859\_0\_20, complet

e sequence.//1.1e-55:543:72//AC003695

F-THYR01001033//Methanobacterium thermoautotrophicum from bases 48264 to 58328 (section 5 of 148) of the complete genome.//0.94:445:58//AE000799

F-THYR01001062//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 199H16, WORKING DRAFT SEQUENCE.//4.4e-45:441:75//AL022320

F-THYR01001093//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//4.9e-34:353:76//AC006241

F-THYR01001100//Human DNA-binding protein mRNA, 3' end.//1.1e-72:742:74//L14787

F-THYR01001120//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-76:521:86//AC005522

F-THYR01001121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 671014, WORKING DRAFT SEQUENCE.//0.00078:594:58//AL031595

F-THYR01001133//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//4.0e-35:349:76//AC004996

F-THYR01001134//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0:154:66//AC005486

F-THYR01001142//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//1.4e-44:374:80//Z82178

F-THYR01001173

F-THYR01001177//Human pigment epithelium-derived factor gene, complete cds.//1.9e-42:250:86//U29953

F-THYR01001189//HS\_3171\_B2\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=20 Row=L, genomic survey sequence.//1.8e-28:246:83//AQ302330

F-THYR01001204//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//4.9e-39:657:64//U34925

F-THYR01001213//, complete sequence.//1.7e-45:257:84//AC005300

F-THYR01001262//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/

28, WORKING DRAFT SEQUENCE.//1.5e-40:274:87//AP000036

F-THYR01001271//*Streptomyces coelicolor* cosmid 1A6.//0.033:364:61//AL023

496

F-THYR01001287//*Drosophila melanogaster* cosmid clone 86E4.//9.6e-49:586:  
69//AL021086

F-THYR01001290//HS\_2045\_B1\_H09\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2045 Col=17 Row=P, genomic survey sequence.//4.4e-13:156:78//AQ248237

F-THYR01001313//*S. lavandulae* bla gene for beta-lactamase, complete cds.  
//1.0:229:64//D12693

F-THYR01001320//*Homo sapiens* Chromosome 22q11.2 PAC Clone p\_n5 In BCRL2-  
GGT Region, complete sequence.//1.1e-88:672:82//AC002472

F-THYR01001321//Human PAC clone DJ527C21 from Xq23, complete sequence.//  
1.2e-115:740:87//AC000114

F-THYR01001322//HS\_3205\_B2\_C12\_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3205 Col=24 Row=F, genomic survey sequence.//0.00031:285:61//AQ304025

F-THYR01001347//*Homo sapiens* mRNA for KIAA0745 protein, partial cds.//2.  
2e-43:638:64//AB018288

F-THYR01001363//*Homo sapiens* PAC clone DJ0845I21 from 7q11.21-q11.23, complete sequence.//1.0e-09:189:74//AC004905

F-THYR01001365//*Homo sapiens* chromosome 10 clone CIT987SK-1163G10 map 10  
q25, complete sequence.//7.6e-168:821:97//AC005660

F-THYR01001374//*Homo sapiens* mRNA for KIAA0707 protein, partial cds.//2.  
3e-155:740:97//AB014607

F-THYR01001401//*Homo sapiens* chromosome 19, cosmid F23149, complete sequence.//3.2e-07:138:73//AC005239

F-THYR01001403//*Homo sapiens* chromosome 12p13.3 clone RPCI3-454B23, WORK  
ING DRAFT SEQUENCE, 48 unordered pieces.//3.6e-70:360:86//AC005845

F-THYR01001405//*Bos taurus* mRNA for NDP52, complete cds.//2.6e-14:559:63  
//AB008852

F-THYR01001406//*Mus musculus* putative steroid dehydrogenase (KIK-I) mRNA  
, complete cds.//1.0e-91:631:82//AF064635

F-THYR01001411//*Homo sapiens* chromosome 19, cosmid F18718, complete sequence.//5.5e-42:509:71//AC006126

F-THYR01001426//\*\*\* SEQUENCING IN PROGRESS \*\*\* *Homo sapiens* genomic DNA  
(PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//  
/2.7e-31:172:81//AJ002553

● F-THYR01001434//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE,  
8 unordered pieces.//1.0:98:70//AC000384

F-THYR01001458//*Bos taurus* non-muscle myosin heavy chain mRNA, partial cds.//1.9e-58:653:71//U87265

F-THYR01001480//*Homo sapiens* clone DJ0756H11, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//7.5e-42:357:80//AC006001

F-THYR01001487//*H. sapiens* DNA sequence.//0.92:160:64//Z22449

F-THYR01001534//*Homo sapiens* chromosome 17, clone hcIT.468\_F\_23, WORKING  
DRAFT SEQUENCE, 3 unordered pieces.//4.8e-47:266:80//AC004666

● F-THYR01001537//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone  
998H6, WORKING DRAFT SEQUENCE.//1.3e-79:479:89//AL031687

F-THYR01001541//Human DNA sequence from clone 399M14 on chromosome Xq26.  
1-26.3. Contains ESTs, an STS and GSSs, complete sequence.//0.0034:106:7  
7//Z96074

F-THYR01001559//*Rattus norvegicus* simple sequence repeat D18Mco6.//1.6e-  
09:351:63//AF006056

F-THYR01001570//RPCI11-49B23.TJ RPCI11 *Homo sapiens* genomic clone R-49B2  
3, genomic survey sequence.//1.4e-65:384:91//AQ052105

F-THYR01001573//*Homo sapiens* clone 24778 unknown mRNA.//8.2e-104:546:95/  
/AF070572

F-THYR01001584//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 23  
65J21, genomic survey sequence.//1.3e-24:180:88//AQ080498

F-THYR01001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone Y313F4, WORKING DRAFT SEQUENCE.//8.7e-145:779:93//AL023808

F-THYR01001602//Homo sapiens chromosome 17, clone hRPK.786\_0\_4, complete  
sequence.//2.9e-26:393:68//AC005863

F-THYR01001605//Dictyostelium discoideum filopodin (talA) gene, complete  
cds.//0.0012:436:58//U14576

F-THYR01001617//Homo sapiens full length insert cDNA clone ZD69D05.//8.6  
e-43:342:82//AF086381

F-THYR01001637//Homo sapiens clone DJ1019E05, WORKING DRAFT SEQUENCE, 10  
unordered pieces.//6.2e-15:318:66//AC004950

F-THYR01001656//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequ  
ence.//1.5e-05:147:68//AC004827

F-THYR01001661

F-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59  
kDa isoform.//2.5e-164:780:98//AJ225089

F-THYR01001673//Homo sapiens clone RG161A02, complete sequence.//4.4e-40  
:770:64//AC005071

F-THYR01001703//S.coelicolor plasmid SCP2 transfer region DNA.//0.14:414  
:59//X72857

F-THYR01001706//Homo sapiens BAC clone RG281B09 from 7q21.1-q31.1, compl  
ete sequence.//2.6e-43:308:75//AC004745

F-THYR01001721//, complete sequence.//9.9e-134:770:91//AC005500

F-THYR01001738//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 355C18, WORKING DRAFT SEQUENCE.//0.99:163:61//AL022327

F-THYR01001745

F-THYR01001746

F-THYR01001772//HS\_3069\_B1\_C05\_MF CIT Approved Human Genomic Sperm Libra

ry D *Homo sapiens* genomic clone Plate=3069 Col=9 Row=F, genomic survey sequence.//1.5e-61:360:91//AQ171021

F-THYR01001793//*B.taurus* mRNA for beta-subunit of rod photoreceptor CNG-channel.//0.028:446:58//X89626

F-THYR01001809

F-THYR01001828//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 110F11, WORKING DRAFT SEQUENCE.//1.3e-175:841:98//AL033526

F-THYR01001854//*Homo sapiens* chromosome 17, clone hCIT54K19, complete sequence.//7.9e-07:445:59//AC003664

F-THYR01001895

4.4e-13:248:68//AB012576

F-THYR01001907//*Homo sapiens* BAC clone RG054D04 from 7q31, complete sequence.//2.9e-15:144:77//AC005058

F-VESEN1000122//HS\_3075\_B1\_C09\_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3075 Col=17 Row=F, genomic survey sequence.//1.1e-16:130:90//AQ143749

F-Y79AA1000013

F-Y79AA1000033//*Homo sapiens* BAC clone GS114I09 from 7p14-p15, complete sequence.//2.9e-95:300:94//AC006027

F-Y79AA1000037//Human prot-oncogene (BMI-1) mRNA, complete cds.//2.4e-19:230:66//L13689

F-Y79AA1000059//*Homo sapiens* immunophilin homolog ARA9 mRNA, complete cds.//2.2e-38:629:64//U78521

F-Y79AA1000065//Human DNA sequence from cosmid J256K24, between markers DXS6791 and DXS8038 on chromosome X contains EST.//5.3e-10:117:83//Z72005

F-Y79AA1000131//*Homo sapiens* LERK-6 (EPLG6) gene, exon 1.//7.6e-10:381:64//U92893

F-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-

25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.4e-165:732:99//AL031864

F-Y79AA1000202//Drosophila melanogaster DNA sequence (P1 DS06882 (D310)) , complete sequence.//9.1e-20:339:65//AC005115

F-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//3.7e-72:397:93//AC004854

F-Y79AA1000230

F-Y79AA1000231//Mus musculus SIK similar protein mRNA, complete cds.//8.5e-151:833:90//AF053232

F-Y79AA1000258//Leishmania donovani histidine secretory acid phosphatase (SAcP-1) gene, complete cds.//0.0099:547:58//U78522

F-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds.//4.0e-11:424:62//AF035207

F-Y79AA1000313

F-Y79AA1000328//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386 A20, genomic survey sequence.//5.9e-07:173:69//B55085

F-Y79AA1000342//RPCI11-57J6.TK.1 RPCI11 Homo sapiens genomic clone R-57J 6, genomic survey sequence.//5.2e-27:151:99//AQ115511

F-Y79AA1000346//B. primigenius mRNA for coat protein gamma-cop.//5.7e-69:694:71//X92987

F-Y79AA1000349//M. musculus Spnr mRNA for RNA binding protein.//1.8e-98:535:92//X84692

F-Y79AA1000355//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-21:129:85//AC005484

F-Y79AA1000368//H. sapiens CpG island DNA genomic Mse1 fragment, clone 12 f1, reverse read cpg12f1.rt1c.//0.00016:53:98//Z56610

F-Y79AA1000405//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P4, WORKING DRAFT SEQUENCE.//0.069:366:59//AL031747

F-Y79AA1000410//Human DNA sequence from PAC 117P19 on chromosome X.//1.0  
e-25:235:80//Z86061

F-Y79AA1000420//H.sapiens CpG island DNA genomic Mse1 fragment, clone 82  
c3, forward read cpg82c3.ft1a.//2.0e-36:194:98//Z63378

F-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 pre  
cursor (Aup1) mRNA, complete cds.//8.5e-121:696:89//U41736

F-Y79AA1000480//HS\_2175\_A2\_H11\_T7 CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2175 Col=22 Row=0, genomic survey  
sequence.//2.5e-26:178:89//AQ307693

● F-Y79AA1000538//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23  
unordered pieces.//0.67:111:72//AC004980

F-Y79AA1000539//HS\_2237\_B2\_F10\_MF CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2237 Col=20 Row=L, genomic survey  
sequence.//1.2e-14:168:77//AQ153503

F-Y79AA1000540//Homo sapiens clone DJ0655N24, WORKING DRAFT SEQUENCE, 8  
unordered pieces.//0.94:127:67//AC005193

F-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//1.7e-114:776:84//X149  
72

● F-Y79AA1000574//M.musculus tex23 mRNA (5' region).//1.8e-23:291:75//X8042  
4

F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence.  
/8.6e-153:755:97//AF091080

F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete  
cds.//5.2e-135:644:98//AF060503

F-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//6.9e-148:902:  
86//X69942

F-Y79AA1000734//Homo sapiens PEX11 beta mRNA for peroxisome assembly fac  
tor, complete cds.//4.8e-180:850:98//AB018080

F-Y79AA1000748//Caenorhabditis elegans cosmid F25B5.//0.00019:308:60//U2

3172

F-Y79AA1000752//Oryctolagus cuniculus mRNA for hnRNP-E1 protein.//1.7e-4

0:513:68//AJ003023

F-Y79AA1000774

F-Y79AA1000782

F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//3.5e-177:847:97//AF098799

F-Y79AA1000794//H.sapiens CpG island DNA genomic Mse1 fragment, clone 45a4, forward read cpg45a4.ft1a.//2.5e-13:104:92//Z61120

● F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds.//0.98:244:60//AF056085

F-Y79AA1000802

F-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//9.3e-76:528:85//U73642

F-Y79AA1000824//RPCI11-26B4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-26B4, genomic survey sequence.//4.4e-14:99:95//B84538

F-Y79AA1000827//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING DRAFT SEQUENCE.//1.5e-08:249:69//AL022315

● F-Y79AA1000833//Macaca fascicularis mRNA for alpha-tubulin.//1.8e-103:603:89//X04757

F-Y79AA1000850

F-Y79AA1000962//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//0.038:468:59//Z82203

F-Y79AA1000966//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.7e-150:865:89//AF071314

F-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//6.4e-122:717:88//U38253

F-Y79AA1000969//Mouse chromosome 6 BAC-284H12 (Research Genetics mouse BAC library) complete sequence.//1.0:155:63//AC002397

F-Y79AA1000976//*Caenorhabditis elegans* cosmid F54C1.//4.3e-06:130:73//U8

8165

F-Y79AA1000985//*Mus musculus* pericentrin mRNA, complete cds.//2.4e-44:42  
8:77//U05823

F-Y79AA1001023

F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds.//2.3e-13:9  
0:100//U63329

F-Y79AA1001048//Human mRNA for very-long-chain acyl-CoA dehydrogenase (V  
LCAD), complete cds.//2.6e-28:772:60//D43682

● F-Y79AA1001061//*Homo sapiens* chromosome 4 clone B331M8 map 4q25, comple  
te sequence.//9.4e-36:292:82//AC004701

F-Y79AA1001068//tipAL-AS complex: tipA=TipAL-AS [*Streptomyces lividans*,  
Genomic, 1146 nt].//0.17:537:59//S64314

F-Y79AA1001077//*Zea mays* mRNA for aldehyde oxidase-2, complete cds.//0.1  
7:231:64//D88452

F-Y79AA1001078

F-Y79AA1001105//Zebrafish otx2 mRNA for otx homeoprotein, complete cds.//  
3.1e-63:529:77//D26173

● F-Y79AA1001145//*Homo sapiens* clone GS166C05, WORKING DRAFT SEQUENCE, 7 u  
nordered pieces.//1.3e-23:228:76//AC005015

F-Y79AA1001167

F-Y79AA1001177//*M. musculus* mRNA for NfiX1-protein.//4.0e-10:398:64//Y076  
88

F-Y79AA1001185//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 169I5, WORKING DRAFT SEQUENCE.//1.1e-113:666:90//Z93015

F-Y79AA1001211//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Libra  
ry D *Homo sapiens* genomic clone Plate=3124 Col=16 Row=P, genomic survey  
sequence.//5.5e-12:87:96//AQ187492

F-Y79AA1001216

F-Y79AA1001228//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//0.028:188:67//AL021841

F-Y79AA1001233//Human placental 17-beta-hydroxysteroid dehydrogenase mRNA, complete cds.//3.5e-24:731:60//M36263

F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)).//1.2e-133:441:97//AJ005892

F-Y79AA1001281//HS\_2241\_B2\_F09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2241 Col=18 Row=L, genomic survey sequence.//5.0e-27:169:94//AQ217497

F-Y79AA1001299//Human Inil mRNA, complete cds.//6.7e-115:323:93//U04847

F-Y79AA1001312

F-Y79AA1001323

F-Y79AA1001384

F-Y79AA1001391//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//5.8e-42:245:74//U59322

F-Y79AA1001394//Caenorhabditis elegans cosmid F54B3, complete sequence.//7.8e-18:636:58//Z48583

F-Y79AA1001402//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-110:738:85//AC005924

F-Y79AA1001493//H.sapiens DNA sequence.//2.0e-27:254:82//Z22497

F-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.1e-158:804:95//AL034430

F-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//1.7e-100:820:78//D14336

F-Y79AA1001541//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//5.1e-28:218:86//AQ150183

F-Y79AA1001548//*Homo sapiens* chromosome 19, cosmid R28738, complete sequence.//5.4e-21:167:86//AC004151

F-Y79AA1001555//*R.norvegicus* mRNA for drebrin A.//0.88:463:59//X59267

F-Y79AA1001581//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//0.00051:252:65//S74494

F-Y79AA1001585//Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds.//7.2e-33:375:76//M26434

F-Y79AA1001594

F-Y79AA1001603//*Homo sapiens* PAC 128M19 derived from chromosome 21q22.3, containing the HMG-14 and CHD5 genes, complete cds, complete sequence.//4.2e-06:338:66//AF064861

F-Y79AA1001613//*Homo sapiens* mRNA for KIAA0683 protein, complete cds.//0.024:520:57//AB014583

F-Y79AA1001647//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\* \* from clone Y53F4, WORKING DRAFT SEQUENCE.//0.014:331:61//Z92860

F-Y79AA1001665//Human DNA sequence from clone 299D3 on chromosome 22q13. 3, complete sequence.//0.99:273:63//Z84468

F-Y79AA1001679//*O.cuniculus* lambda-crystallin mRNA, complete cds.//1.2e-97:682:81//M22743

F-Y79AA1001692//insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1292 nt, segment 1 of 4].//5.6e-05:426:59//S37712

F-Y79AA1001696//Rice endogenous double-stranded RNA encoding polyprotein (containing putative helicase and putative RNA-dependent RNA polymerase domains), complete cds.//1.0:437:60//D32136

F-Y79AA1001705//*M.musculus* fkh-5 gene.//0.18:153:64//X71943

F-Y79AA1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//5.4e-76:191:98//AL022240

F-Y79AA1001781//*Homo sapiens* genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 10/15, WORKING DRAFT SEQUENCE.//0.99:227:63//AP0000

17

F-Y79AA1001805//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13  
d12, reverse read cpg13d12.rt1c.//2.6e-13:88:100//Z64565

F-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds.//3.7e-130  
:775:88//U74297

F-Y79AA1001846//CIT-HSP-2300M6.TR CIT-HSP Homo sapiens genomic clone 230  
0M6, genomic survey sequence.//8.3e-17:218:76//AQ012369

F-Y79AA1001848//Human mRNA for KIAA0390 gene, complete cds.//4.2e-10:378  
:62//AB002388

F-Y79AA1001866//Rattus norvegicus Cys2/His2 zinc finger protein (rKr1) m  
RNA, complete cds.//6.9e-41:441:71//U41164

F-Y79AA1001874//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spl  
iced isoform of Jagged2, complete cds.//0.00017:412:62//AF029779

F-Y79AA1001875//CIT-HSP-2317G18.TR CIT-HSP Homo sapiens genomic clone 23  
17G18, genomic survey sequence.//1.9e-09:271:67//AQ042654

F-Y79AA1001923//H.sapiens CpG island DNA genomic Mse1 fragment, clone 19  
3c12, forward read cpg193c12.ft1a.//0.0031:108:75//Z60186

F-Y79AA1001963//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2  
510J4, genomic survey sequence.//1.8e-05:56:100//AQ261184

F-Y79AA1002027//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UB  
C17) mRNA, complete cds.//3.3e-13:451:62//AF028340

F-Y79AA1002083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 526I14, WORKING DRAFT SEQUENCE.//0.91:134:65//Z82214

F-Y79AA1002089

F-Y79AA1002093//Mus musculus transcription factor like protein 4 TCFL4 m  
RNA, partial cds.//1.2e-112:678:88//U43548

F-Y79AA1002103//HS\_3052\_B1\_H08\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3052 Col=15 Row=P, genomic survey  
sequence.//6.5e-18:238:72//AQ135014

F-Y79AA1002115

F-Y79AA1002125//H.sapiens (D8S135) DNA segment containing GT repeat.//1.

5e-14:99:96//X61693

F-Y79AA1002139//Saccharomyces cerevisiae dnaJ homolog Hlj1p (HLJ1) gene, complete cds.//2.5e-07:208:64//U19358

F-Y79AA1002204//HS\_2235\_B2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=24 Row=H, genomic survey sequence.//2.9e-13:89:98//AQ154260

F-Y79AA1002208//CIT-HSP-2006M21.TV CIT-HSP Homo sapiens genomic clone 20 06M21, genomic survey sequence.//3.7e-27:154:98//B56397

F-Y79AA1002209//E.coli tyrS gene coding for tyrosyl-tRNA synthetase.//2. 8e-05:143:70//J01719

F-Y79AA1002210//Homo sapiens chromosome 19, cosmid R28058, complete sequence.//8.3e-22:229:78//AC005615

F-Y79AA1002211//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.0e-06:241:67//AC003043

F-Y79AA1002220//CIT-HSP-2374P23.TR CIT-HSP Homo sapiens genomic clone 23 74P23, genomic survey sequence.//1.3e-68:375:95//AQ109738

F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds.//0.12:203:63 //D42045

F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//1. 3e-174:821:98//AB014592

F-Y79AA1002246//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unorderd pieces.//0.50:470:60//AC005015

F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds.//6. 8e-159:748:98//AB014555

F-Y79AA1002298//Human density enhanced phosphatase-1 mRNA, complete cds. //0.036:278:62//U10886

F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//6.

4e-129:622:97//AB014534

F-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.0e-116:693:82//X67877

F-Y79AA1002351//S.clavuligerus pah and cas genes.//1.0:369:58//X84101

F-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-sub unit).//5.4e-105:762:80//Y18208

F-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//1.0e-159:411:100//AC005920

F-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//1.1e-118:609:84//AC004662

F-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//4.4e-90:529:88//U49385

F-Y79AA1002431//Chlamydomonas reinhardtii novel protein kinase mRNA, complete cds.//1.0:166:66//U36196

F-Y79AA1002433//CIT-HSP-384K8.TF CIT-HSP Homo sapiens genomic clone 384K8, genomic survey sequence.//0.24:85:72//B51917

F-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.9e-13:242:69//AC006116

F-Y79AA1002482//Homo sapiens full length insert cDNA clone ZC18H06.//1.2e-35:462:71//AF088022

F-Y79AA1002487//Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].//0.93:215:60//X94677

【0833】

相同性検索結果データ3.

3'末端クローン配列に対するESTとSTSを除いたGenBank相同性検索結果データ

各データは、

クローン配列名、

トップヒットデータのDefinition、

P値:比較配列の長さ (base):相同性(%)、

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、同一クローンで5'末端配列に対応する3'末端配列が決定されていないものは空欄とした。相同性のスコアのP値が1より大であった場合はデータは示さない。

R-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds  
.//3.6e-60:504:78//L16953

R-HEMBA1000030//F.rubripes GSS sequence, clone 063K10bD3, genomic survey  
sequence.//0.28:117:68//Z88864

R-HEMBA1000042//RPCI11-77G23.TV RPCI11 Homo sapiens genomic clone R-77G2  
3, genomic survey sequence.//1.3e-56:292:97//AQ268240

R-HEMBA1000046//Homo sapiens chromosome X map Xq28, complete sequence.//  
9.8e-56:401:82//U82696

R-HEMBA1000050//Human cosmid insert containing polymorphic marker DXS455  
.//0.0010:175:68//L31948

R-HEMBA1000076//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6  
unordered pieces.//4.9e-41:364:79//AC005520

R-HEMBA1000111//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human B  
AC library) complete sequence.//4.7e-30:229:84//AC003684

R-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete se  
quence.//2.4e-93:503:93//AC003104

R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//6.  
5e-99:514:94//AB018340

R-HEMBA1000150//Homo sapiens clone RG086D03, WORKING DRAFT SEQUENCE, 3 u  
nordered pieces.//2.7e-37:289:83//AC005060

R-nnnnnnnnnnnnnnn//Homo sapiens scaffold attachment factor B (SAF-B) mRNA,  
partial cds.//3.1e-21:417:64//L43631

R-HEMBA1000158

R-nnnnnnnnnnnnnnn

R-HEMBA1000180//Plasmodium falciparum encoding Pfg27/25.//0.073:292:56//

X84904

R-HEMBA1000185//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7  
unordered pieces.//5.3e-40:286:85//AC006146

R-HEMBA1000193

R-HEMBA1000201//Homo sapiens SNF5/INI1 gene, exon 9.//2.0e-24:137:99//Y1  
7126

R-HEMBA1000213//Caenorhabditis elegans cosmid C44C8.//0.025:192:68//AF10  
0655

R-HEMBA1000216//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete  
sequence.//2.5e-31:269:79//AF001548

R-nnnnnnnnnnnnn

R-HEMBA1000231//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1  
p35. Contains delta opiate receptor, CpG island, CA repeat,.//4.3e-24:40  
0:68//AL009181

R-HEMBA1000243//Homo sapiens chromosome 17, Neurofibromatosis 1 locus,  
complete sequence.//1.3e-19:319:69//AC004526

R-HEMBA1000244

R-HEMBA1000251//Meloidogyne hapla mitochondrial COII gene, 3' end of cds  
; transfer RNA-His gene; 16S ribosomal RNA gene; ND3 gene, complete cds;  
cytochrome b (cytb) gene, 5' end of cds.//0.16:338:60//L76262

R-HEMBA1000264//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndr  
ome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.00093:300:66//AP00  
0012

R-nnnnnnnnnnnnn//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human  
BAC library) complete sequence.//3.5e-10:238:70//AC003037

R-HEMBA1000282//Arabidopsis thaliana BAC IG002P16.//0.71:344:60//AF00727  
0

R-HEMBA1000288//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 compl  
ete sequence.//4.8e-33:267:82//AC003046

R-HEMBA1000290//*Homo sapiens* chromosome 17, clone HRPC837J1, complete sequence.//2.2e-15:249:69//AC004223

R-HEMBA1000302//CIT-HSP-2173N10.TF CIT-HSP *Homo sapiens* genomic clone 21 73N10, genomic survey sequence.//1.0:215:61//B95105

R-nnnnnnnnnnnnn//*Mus musculus* Plenty of SH3s (POSH) mRNA, complete cds.//1.0e-77:551:82//AF030131

R-nnnnnnnnnnnnn//*Rattus norvegicus* Ca2+-dependent activator protein (CAPS) mRNA, complete cds.//2.0e-96:546:90//U16802

R-HEMBA1000307//*Mus musculus* mRNA for CDV-1 protein.//3.8e-36:315:68//Y1 0496

R-nnnnnnnnnnnnn//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.078:379:59//AC 005505

R-HEMBA1000338//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//2.0e-33:399:72//AL031667

R-HEMBA1000351//*Homo sapiens* complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//1.7 e-39:272:87//AJ003147

R-HEMBA1000355//Human primary Alu transcript.//0.0045:67:85//U67829

R-HEMBA1000357//*Homo sapiens* (subclone 9\_h8 from P1 H16) DNA sequence.//8.7e-93:426:88//L42086

R-HEMBA1000366//*Homo sapiens* PAC clone DJ0942I16 from 7q11, complete sequence.//1.7e-12:130:83//AC006012

R-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12 .3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//1.9e-69:355:97//AL031587

R-HEMBA1000376//*Homo sapiens* chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//3.7e-66:410:89//AC006116

R-HEMBA1000387//*Homo sapiens* chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:363:81//AC002993

R-HEMBA1000390//*Homo sapiens* BAC clone RG041D11 from 7q21, complete sequence.//4.6e-23:417:69//AC005053

R-HEMBA1000392//Human Chromosome 11p14.3 PAC clone pDJ59m18, complete sequence.//6.2e-05:174:68//AC004582

R-HEMBA1000396//*Homo sapiens* DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//1.4e-62:564:77//AL022575

R-HEMBA1000411

R-HEMBA1000418//Liverwort *Marchantia polymorpha* chloroplast genome DNA.//0.94:210:60//X04465

R-HEMBA1000422//CIT-HSP-2382A6.TR CIT-HSP *Homo sapiens* genomic clone 2382A6, genomic survey sequence.//4.4e-12:98:92//AQ078233

R-HEMBA1000428//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains CSSs, complete sequence.//2.0e-93:526:90//Z95400

R-HEMBA1000434//*Homo sapiens* clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-07:452:60//AC004826

R-HEMBA1000442//*E. caballus* microsatellite DNA, clone HMB4.//0.39:135:62//Y07733

R-HEMBA1000456//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence.//2.6e-05:174:70//AL010226

R-HEMBA1000459//*Arabidopsis thaliana* putative transmembrane protein G1p (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (AT EM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), putative acyl-coA dehydrogenase (AtG6), and calcium dependent protein kinase genes, complete cds; and unknown genes.//0.013:212:63//AF049236

R-HEMBA1000460//*Homo sapiens* PAC clone DJ0593H12 from 7p31, complete seq

uence.//8.6e-114:556:98//AC004839

R-HEMBA1000464//*Caenorhabditis elegans* cosmid C34B7, complete sequence.//0.086:334:61//Z83220

R-HEMBA1000469//*Homo sapiens* BAC clone RG442F18 from 2, complete sequence.//1.8e-52:472:79//AC005104

R-HEMBA1000488//, complete sequence.//3.3e-68:200:99//AC005500

R-HEMBA1000490//*Caenorhabditis elegans* cosmid Y53C12B, complete sequence.//0.97:233:61//Z99278

R-HEMBA1000491

● R-HEMBA1000504//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-64, complete sequence.//1.7e-08:440:60//AL009014

R-HEMBA1000505//*Homo sapiens* genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11.//0.37:189:62//AB020858

R-HEMBA1000508//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//1.1e-25:248:80//Z70280

R-HEMBA1000518//RPCI11-6022.TV RPCI-11 *Homo sapiens* genomic clone RPCI-11-6022, genomic survey sequence.//0.0035:293:61//B49544

R-HEMBA1000519

● R-HEMBA1000520//*Arabidopsis thaliana* chromosome II BAC F10A12 genomic sequence, complete sequence.//0.30:255:63//AC006232

R-HEMBA1000523//Human cleavage stimulation factor 77kDa subunit mRNA, complete cds.//1.2e-53:203:92//U15782

R-HEMBA1000531//CIT-HSP-388J17.TR CIT-HSP *Homo sapiens* genomic clone 388J17, genomic survey sequence.//2.7e-24:137:99//B55638

R-HEMBA1000540//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044

R-HEMBA1000545//*Homo sapiens* Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.//6.9e-87:552:87//AC004103

R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE.//8.9e-121:584:98//AL034555

R-HEMBA1000557//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//5.7e-45:307:87//AC004381

R-HEMBA1000561//Mus musculus clone OST20235, genomic survey sequence.//1.3e-43:279:90//AF046762

R-HEMBA1000563//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//3.8e-05:506:56//AE001368

R-HEMBA1000568//RPCI11-49P8.TK.1 RPCI11 Homo sapiens genomic clone R-49P8, genomic survey sequence.//1.7e-101:498:97//AQ116293

R-nnnnnnnnnnnn

R-HEMBA1000575//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 754E20, WORKING DRAFT SEQUENCE.//1.3e-47:458:75//AL022335

R-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.9e-62:447:81//AF045573

R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.2e-111:591:94//AJ007509

R-HEMBA1000592//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence.//3.5e-09:421:60//AL010216

R-HEMBA1000594//Homo sapiens clone RG004N09, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-15:421:66//AC005044

R-HEMBA1000604//HS\_2220\_A1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=19 Row=M, genomic survey sequence.//1.0e-51:306:92//AQ151991

R-HEMBA1000608

R-HEMBA1000622//H.sapiens CpG island DNA genomic Mse1 fragment, clone 155e4, reverse read cpg155e4.rt1a.//4.5e-16:105:98//Z56962

R-HEMBA1000636//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//4.8e-62:421:86//AP00

0008

R-HEMBA1000637//*Homo sapiens* mRNA for KIAA0690 protein, partial cds.//1.

2e-97:443:97//AB014590

R-HEMBA1000655//*Homo sapiens* chromosome 19, cosmid R26349, complete sequence.//9.8e-61:311:90//AC005953

R-HEMBA1000657

R-HEMBA1000662

R-HEMBA1000673//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//1.0e-13:351:63//Z97196

● R-HEMBA1000682//*Homo sapiens* clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-50:298:79//AC005377

R-HEMBA1000686//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00048:210:62//AQ093513

R-HEMBA1000702//*Homo sapiens* clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.7e-54:317:88//AC005000

R-HEMBA1000705//*Glossonotus univittatus* 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//0.080:138:65//U77

850

● R-HEMBA1000719//*Rattus norvegicus* mRNA for TESK1, complete cds.//0.96:29 1:58//D50864

R-HEMBA1000722

R-HEMBA1000726//*Homo sapiens* PAC clone DJ0701016 from 7q33-q36, complete sequence.//4.4e-26:284:77//AC005531

R-HEMBA1000727//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete sequence.//9.1e-05:351:60//AL010266

R-HEMBA1000747//*Homo sapiens* DNA sequence from PAC 124C6 on chromosome 6 q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.5e-16:123:93//AL021326

R-HEMBA1000749//Human Chromosome 16 BAC clone CIT987SK-327024, complete sequence.//2.8e-32:298:79//AC003108

R-HEMBA1000752//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-90:542:90//Z92545

R-HEMBA1000769//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-36:405:75//AC005031

R-HEMBA1000773//HS\_3050\_A2\_B08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=16 Row=C, genomic survey sequence.//0.00053:268:60//AQ105619

R-HEMBA1000774//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//4.7e-46:338:85//AC004690

R-HEMBA1000791//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//5.3e-47:279:91//U14571

R-HEMBA1000817//Sequence 1 from Patent WO 8904839.//0.86:148:67//I09339

R-HEMBA1000822//T.brucei kinetoplast maxicircle variable region DNA.//0.00061:246:61//Z15118

R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM 160) mRNA, complete cds.//6.9e-43:228:98//AF048977

R-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.7e-41:319:84//AL022394

R-HEMBA1000851//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.40:168:67//AC004260

R-HEMBA1000852//*Homo sapiens* Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.5e-112:572:96//AC005295

R-HEMBA1000867//*Homo sapiens* clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//0.11:121:71//AC004938

R-HEMBA1000869//*Homo sapiens* chromosome 16p11.2 BAC clone CIT987SK-A-180 G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-22:186:76//AC00204 2

R-HEMBA1000870//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//0.0060:283:63//AC002528

R-HEMBA1000872//*Rattus norvegicus* polymorphic satellite repetitive elements.//3.8e-05:269:61//M98801

R-HEMBA1000876//*Homo sapiens* chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-38:327:77//AC006057

R-HEMBA1000908//CIT-HSP-2373I4.TR CIT-HSP *Homo sapiens* genomic clone 237 3I4, genomic survey sequence.//5.0e-34:221:90//AQ108658

R-HEMBA1000910//*T. pigmentosa* UM1060 macronuclear rDNA telomeric region 3 ' term.//0.19:280:61//X04205

R-HEMBA1000918//RPCI11-68E14.TK RPCI11 *Homo sapiens* genomic clone R-68E1 4, genomic survey sequence.//1.3e-32:172:100//AQ267293

R-HEMBA1000919

R-HEMBA1000934//*Homo sapiens* DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.6e-18:284:71//AL021997

R-HEMBA1000942//*Homo sapiens* clone RG350L10, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.4e-17:217:76//AC005098

R-HEMBA1000943//*Homo sapiens* chromosome 17, clone hRPK.640\_I\_15, complete sequence.//9.0e-113:586:95//AC005324

R-HEMBA1000946//T5N8TFB TAMU *Arabidopsis thaliana* genomic clone T5N8, genomic survey sequence.//0.030:369:59//B26224

R-HEMBA1000960//*Homo sapiens* clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-52:494:77//AC005096

R-HEMBA1000968//*Homo sapiens* P1 clone 797a11 containing MHC class II DQ-beta (HLA-DQB) and MHC class II DC-alpha (HLA-DCA) genes, complete cds.//3.5e-77:568:83//U92032

R-HEMBA1000971//RPCI11-54D1.TJ RPCI11 *Homo sapiens* genomic clone R-54D1, genomic survey sequence.//2.3e-27:153:98//AQ081552

● R-HEMBA1000972//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//7.3e-43:375:79//AL023876

R-HEMBA1000974//*Homo sapiens* clone DA0091H08, complete sequence.//2.8e-104:521:97//AC004817

R-HEMBA1000975//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//8.0e-22:352:68//AL031311

R-HEMBA1000985//*Homo sapiens* PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-05:306:63//AC004888

● R-HEMBA1000986//*Homo sapiens* clone RG031N19, WORKING DRAFT SEQUENCE, 10 unordered pieces.//5.7e-37:296:83//AC005632

R-HEMBA1000991//RPCI11-22017.TVB RPCI-11 *Homo sapiens* genomic clone RPCI-11-22017, genomic survey sequence.//6.5e-44:162:90//AQ008952

R-HEMBA1001007

R-HEMBA1001008//*Homo sapiens* chromosome 16, P1 clone 79-2A (LANL), complete sequence.//0.082:313:60//AC005365

R-HEMBA1001009//*O. sativa* osr40g2 gene.//0.99:203:62//Y08987

R-HEMBA1001017//*Homo sapiens* mRNA for KIAA0468 protein, complete cds.//1.0e-113:587:95//AB007937

R-HEMBA1001019//*Bos taurus* cyclin-dependent kinase 1 (cdk1/cdc2) mRNA, c

omplete cds.//7.4e-24:215:82//L26547

R-HEMBA1001020//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//2.8e-18:449:64//AL008722

R-HEMBA1001022

R-HEMBA1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//6.6e-48:536:74//AF070717

R-HEMBA1001026//T33H14TF TAMU *Arabidopsis thaliana* genomic clone T33H14, genomic survey sequence.//0.013:180:66//B97363

R-nnnnnnnnnnnn//*Caenorhabditis elegans* cosmid R10H10, complete sequence.//1.2e-25:438:65//Z70686

R-HEMBA1001051//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.3e-38:188:89//AC004217

R-HEMBA1001052//Rabbit alpha-1-globin gene to theta-1-globin pseudogene region.//2.4e-24:279:74//X04751

R-HEMBA1001060//HS\_2056\_B1\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=1 Row=F, genomic survey sequence.//4.1e-14:137:83//AQ245004

R-HEMBA1001071//*M. musculus* COL3A1 gene for collagen alpha-I.//6.9e-38:513:70//X52046

R-HEMBA1001077//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//1.9e-22:507:61//AL022318

R-HEMBA1001080

R-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.2e-43:317:83//AC004586

R-HEMBA1001088//*Caenorhabditis elegans* cosmid C18H7.//0.46:301:60//AF067607

R-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//5.3e-98

:501:96//AC005105

R-HEMBA1001099

R-HEMBA1001109//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING DRAFT SEQUENCE.//3.1e-39:335:80//AL033527

R-HEMBA1001121//Human cosmid LL12NC01-132B11A, ETV6 gene, intron 2.//9.8e-11:122:81//U81833

R-HEMBA1001122//Plasmodium falciparum MAL3P6, complete sequence.//0.0024:284:63//Z98551

R-HEMBA1001123//Human NFE genomic fragment.//3.6e-26:318:72//M98511

R-HEMBA1001133

R-HEMBA1001137//Homo sapiens full length insert cDNA clone ZD29F04.//4.2e-88:426:98//AF086241

R-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-41:304:84//AC005077

R-HEMBA1001172//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//3.7e-36:261:85//Z98304

R-HEMBA1001174//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.0:219:58//AE001398

R-HEMBA1001197

R-HEMBA1001208//HS\_2233\_A1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=19 Row=M, genomic survey sequence.//0.083:174:68//AQ170789

R-HEMBA1001226//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-59:553:75//AC005377

R-HEMBA1001235//RPCI11-50E6.TJ RPCI11 Homo sapiens genomic clone R-50E6, genomic survey sequence.//2.6e-08:97:76//AQ052666

R-HEMBA1001247//Caenorhabditis elegans cosmid C01F1.//2.4e-05:319:63//U58761

R-HEMBA1001257//Rattus norvegicus alpha-methylacyl-CoA racemase mRNA, co

mplete cds.//1.5e-24:439:66//U89905

R-HEMBA1001265//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//9.9e-21:537:63//AC004491

R-nnnnnnnnnnnnn//Homo sapiens chromosome 17, clone HCIT75G16, complete sequence.//0.022:169:65//AC003042

R-HEMBA1001286

R-HEMBA1001289

R-HEMBA1001294//HS\_3219\_A2\_G01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=2 Row=M, genomic survey sequence.//0.24:251:63//AQ189882

R-HEMBA1001299//Homo sapiens, clone hRPK.12\_A\_1, complete sequence.//1.3e-38:381:76//AC006222

R-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//4.1e-28:114:92//E12258

R-HEMBA1001303//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00011:382:58//AL031744

R-HEMBA1001310

R-HEMBA1001319//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-09:491:58//AC005504

R-HEMBA1001323//Drosophila yakuba mitochondrial DNA molecule.//8.3e-06:485:60//X03240

R-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//2.2e-14:277:69//AL021

R-HEMBA1001327//Human DNA sequence from clone 522P13 on chromosome 6p21.

31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.15:360:61//AL024509

R-HEMBA1001330//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-27:481:67//AC004216

R-HEMBA1001351//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//7.1e-45:252:94//AC006238

R-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//1.4e-113:569:97//AC006241

R-HEMBA1001375//Homo sapiens full length insert cDNA clone ZE09H03.//2.8e-89:428:99//AF086542

R-HEMBA1001377//Homo sapiens PAC clone DJ0728D04, complete sequence.//2.3e-32:324:77//AC004865

R-HEMBA1001383

R-HEMBA1001387

R-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces.//8.9e-06:108:83//AC005073

R-HEMBA1001391//Yeast mitochondrial aap1 gene for ATPase subunit 8.//7.3e-08:500:59//X00960

R-HEMBA1001398//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//2.3e-48:315:88//AP000050

R-HEMBA1001405//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.//5.5e-35:464:68//AL034380

R-HEMBA1001407

R-HEMBA1001411//Yeast (S.cerevisiae) mitochondria Ser-tRNA-UCN gene and flanks.//0.00029:301:62//K01981

R-HEMBA1001413

R-HEMBA1001415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c

lone 41018, WORKING DRAFT SEQUENCE.//5.6e-101:512:96//AL031732

R-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7  
unordered pieces.//6.3e-37:302:81//AC006146

R-HEMBA1001433//Human DNA sequence from PAC 339A18 on chromosome Xp11.2.  
Contains KIAA0178 gene, similar to mitosis-specific chromosome segregat  
ion protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1,  
ESTs and STS.//1.9e-32:242:79//Z97054

R-HEMBA1001435//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) re  
lated locus, complete sequence.//5.7e-59:457:82//AC004527

● R-HEMBA1001442//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-  
27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STS  
s and a polymorphic CA repeat.//0.051:276:63//Z98950

R-HEMBA1001446//HS\_3207\_A1\_A08\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3207 Col=15 Row=A, genomic survey  
sequence.//8.9e-06:119:73//AQ175385

R-HEMBA1001450//Homo sapiens BAC clone RG114B19 from 7q31.1, complete se  
quence.//0.0043:266:63//AC005065

R-HEMBA1001454//Homo sapiens PAC clone DJ0673011 from 7q31, complete seq  
uence.//7.1e-25:210:82//AC004855

● R-HEMBA1001455//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complet  
e sequence.//2.7e-08:316:62//AC005324

R-HEMBA1001463//Homo sapiens chromosome 17, clone hRPK.1064\_E\_11, comple  
te sequence.//0.57:219:60//AC005208

R-HEMBA1001476//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12  
unordered pieces.//9.3e-50:252:80//AC004840

R-HEMBA1001478

R-HEMBA1001497

R-HEMBA1001510//Human HLA class III region containing cAMP response elem  
ent binding protein-related protein (CREB-RP) and tenascin X (tenascin-X

) genes, complete cds, complete sequence.//3.5e-41:282:86//U89337

R-HEMBA1001515//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//1.9e-79:529:86//Z98753

R-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//4.3e-18:335:71//AC004549

R-HEMBA1001522

R-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands.//5.6e-08:265:67//Z98258

● R-HEMBA1001533//Human DNA sequence from PAC 179M20 on chromosome 20q12-1  
3.1. Contains adenosine deaminase (ADA), placental protein Diff33, CA repeat, ESTs, STS.//7.8e-16:235:72//Z97053

R-HEMBA1001557

R-HEMBA1001566//Human Chromosome X clone bWxD187, complete sequence.//2.  
2e-44:416:78//AC004383

R-HEMBA1001569//Sequence 15 from patent US 5693476.//1.8e-59:389:88//I77  
040

R-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//1.1e-44:316:87//AC004453

● R-HEMBA1001579//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0047:437:60//A  
C005506

R-HEMBA1001581//P.falciparum complete gene map of plastid-like DNA (IR-B).//2.3e-07:491:58//X95276

R-HEMBA1001585//Caenorhabditis elegans cosmid C06A6.//0.68:224:62//U4101

2

R-HEMBA1001589

R-HEMBA1001595//CIT-HSP-2349G19.TF CIT-HSP Homo sapiens genomic clone 23  
49G19, genomic survey sequence.//8.0e-69:337:99//AQ060483

R-HEMBA1001608//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//9.5e-59:514:78//AC005177

R-HEMBA1001620//S.polyrrhiza mRNA for D-myo-inositol-3-phosphate synthase.//4.5e-12:289:65//Z11693

R-nnnnnnnnnnnnnn//HS\_2195\_A1\_E09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=17 Row=I, genomic survey sequence.//5.8e-09:358:58//AQ292688

R-HEMBA1001636//Human putative potassium channel subunit (h-erg) mRNA, complete cds.//0.77:225:59//U04270

● R-HEMBA1001640//Human DNA sequence from PAC 50J22 on chromosome 6p21. Contains ETS related protein TEL like and GS2 like genes, ESTs and an STS. //6.0e-49:404:79//Z84484

R-nnnnnnnnnnnnnn

R-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.1e-103:532:95//AC005368

R-HEMBA1001658//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.0:197:64//AL023808

R-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.5e-100:457:93//AC005740

● R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//1.2e-90:496:91//AF072247

R-HEMBA1001675

R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds.//1.3e-101:534:94//AF038962

R-HEMBA1001681//CIT-HSP-2345M7.TF CIT-HSP Homo sapiens genomic clone 2345M7, genomic survey sequence.//0.21:124:68//AQ056593

R-HEMBA1001702//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//8.3e-06:279:63//AC004801

R-HEMBA1001709//*Homo sapiens* mRNA for KIAA0698 protein, complete cds.//1  
.9e-96:483:96//AB014598

R-HEMBA1001711//Human HepG2 3' region cDNA, clone hmd2b02.//2.3e-31:169:  
100//D16886

R-HEMBA1001712//HS-1015-B1-E01-MR.abi CIT Human Genomic Sperm Library C  
*Homo sapiens* genomic clone Plate=CT 790 Col=1 Row=J, genomic survey sequ  
ence.//0.0025:200:65//B32577

R-HEMBA1001714//*Rattus norvegicus* mitochondrial ATPase inhibitor gene, c  
omplete cds.//6.6e-27:316:75//U12250

● R-HEMBA1001718//CIT-HSP-2171J2.TR CIT-HSP *Homo sapiens* genomic clone 217  
1J2, genomic survey sequence.//3.1e-41:167:87//B89781

R-HEMBA1001723//*Rattus norvegicus* EH domain binding protein Epsin mRNA,  
complete cds.//0.53:275:61//AF018261

R-HEMBA1001731//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 322P7, WORKING DRAFT SEQUENCE.//2.9e-48:292:84//AL023799

R-HEMBA1001734//*Homo sapiens* Chromosome 15q22.3-23 PAC 88m3, WORKING DRA  
FT SEQUENCE, 2 ordered pieces.//3.2e-33:290:81//AC005959

● R-HEMBA1001744//Human DNA sequence from clone 134E15 on chromosome 6q21  
Contains Blimp-1, apoptosis specific protein similar to yeast APG5 ESTs,  
GSSs and retroviral sequence, complete sequence.//0.98:203:62//AL022067

R-HEMBA1001745//*Homo sapiens* BAC clone RG298G08 from 7p15-p21, complete  
sequence.//0.00019:312:59//AC005084

R-HEMBA1001746//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC812 genomic  
sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.045:457:61//AC  
004153

R-HEMBA1001761//*Homo sapiens* chromosome X, clone hCIT.200\_L\_4, complete  
sequence.//3.8e-39:331:80//AC006121

R-HEMBA1001781//*Homo sapiens* Xp22 BAC GSHB-590J6 (Genome Systems Human B  
AC library) complete sequence.//0.0062:245:60//AC004554

R-HEMBA1001784//*Homo sapiens* chromosome 5p, BAC clone 50g21 (LBNL H154),  
complete sequence.//2.1e-22:370:63//AC005740

R-HEMBA1001791//Human DNA sequence from clone 931E15 on chromosome Xq25.  
Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0  
e-50:408:80//AL023575

R-HEMBA1001800//CIT-HFP-2049N5.TF CIT-HSP *Homo sapiens* genomic clone 204  
9N5, genomic survey sequence.//9.0e-37:335:77//AQ009222

R-HEMBA1001803//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC357 genomic  
sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.86:536:56//AC0  
05506

R-nnnnnnnnnnnnn//*Mouse interleukin 2 receptor* (p55 IL-2R) mRNA, 5' end.//  
2.9e-93:553:89//M21977

R-HEMBA1001808//*Homo sapiens* mRNA, chromosome 1 specific transcript KIAA  
0500.//2.8e-112:548:98//AB007969

R-HEMBA1001809

R-HEMBA1001815//*Homo sapiens* Xp22 BAC GS-321G17 (Genome Systems Human BA  
C library) complete sequence.//2.6e-48:363:84//AC004025

R-HEMBA1001819//*Homo sapiens* \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 157  
7, WORKING DRAFT SEQUENCE.//1.1e-15:275:68//AJ009612

R-HEMBA1001820//HS\_3022\_B1\_A09\_T7 CIT Approved Human Genomic Sperm Libra  
ry D *Homo sapiens* genomic clone Plate=3022 Col=17 Row=B, genomic survey  
sequence.//0.00054:335:59//AQ165107

R-nnnnnnnnnnnnn//*Xenopus laevis* intersectin mRNA, complete cds.//1.4e-19:  
533:63//AF032118

R-HEMBA1001824//*S. claviger* linear plasmid pSCL (complete sequence)./  
/0.62:189:65//X54107

R-HEMBA1001835//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 191J18, WORKING DRAFT SEQUENCE.//1.0:450:60//AL024507

R-HEMBA1001844//Human familial Alzheimer's disease (STM2) gene, complete

cds.//1.6e-07:170:68//U50871  
R-HEMBA1001847  
R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//3  
.3e-108:553:96//AB014517  
R-HEMBA1001864//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A1  
6, genomic survey sequence.//1.7e-14:245:67//AG002463  
R-HEMBA1001866//HS\_2258\_B2\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=H, genomic survey sequence.//2.8e-39:397:75//AQ221138  
R-nnnnnnnnnnnnnnnnnnn//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//5.9e-56:303:94//AC005065  
R-HEMBA1001888//Homo sapiens Xp22-150 BAC GSMB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.7e-43:281:88//AC006210  
R-HEMBA1001896  
R-HEMBA1001910  
R-HEMBA1001912//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//0.10:307:61//AC004775  
R-HEMBA1001913  
R-HEMBA1001915//HS\_2037\_A1\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=23 Row=I, genomic survey sequence.//0.071:206:64//AQ233106  
R-HEMBA1001918//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//0.97:449:59//AC004775  
R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.0e-105:534:96//AF000145  
R-HEMBA1001939//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//4.6e-13:120:82//AL021707  
R-HEMBA1001940//Homo sapiens clone DJ1093I16, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-36:301:81//AC005629

R-HEMBA1001942//Human PAC clone DJ0205E24 from Xq23, complete sequence./  
/1.9e-10:208:68//AC003013

R-HEMBA1001945//Plasmodium falciparum chromosome 2, section 70 of 73 of  
the complete sequence.//1.2e-06:393:60//AE001433

R-HEMBA1001950//R.prowazekii genomic DNA fragment (clone A437R).//0.33:1  
22:66//Z82646

R-HEMBA1001960//Borrelia afzelii VS461 outer surface protein D (ospD) ge  
ne, complete cds.//0.0086:427:59//U05329

R-HEMBA1001962//Homo sapiens chromosome 4 clone B71M12 map 4q25, comple  
te sequence.//4.5e-07:176:70//AC004069

R-HEMBA1001964//HS\_2215\_B1\_H01\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2215 Col=1 Row=P, genomic survey s  
equence.//7.3e-25:215:74//AQ151931

R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.  
2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive iso  
log of a Rat gene) and a novel alternatively spliced gene. Contains a pu  
tative CpG island, ESTs and GSSs, complete sequence.//1.7e-51:209:95//AL  
031178

R-HEMBA1001979//CIT-HSP-2387I12.TF.1 CIT-HSP Homo sapiens genomic clone  
2387I12, genomic survey sequence.//4.9e-06:153:71//AQ240461

R-HEMBA1001987//Human DNA sequence from clone 444C7 on chromosome 6p22.3  
-23. Contains an EST, an STS and GSSs, complete sequence.//3.1e-46:437:7  
7//AL033521

R-HEMBA1001991//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1  
p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatases  
-1, ESTs, and a CA repeat.//1.1e-48:446:78//AL020997

R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta).//5.  
1e-90:448:97//AJ005801

R-HEMBA1002008//Homo sapiens DNA sequence from PAC 95C20 on chromosome X

p11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//3.2e-42:317:84//Z97181

R-HEMBA1002018//HS\_3006\_B1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=19 Row=H, genomic survey sequence.//1.0:63:74//AQ089717

R-HEMBA1002022//Homo sapiens chromosome 18, clone hRPK.453\_M\_1, complete sequence.//0.93:339:59//AC006203

R-HEMBA1002035//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.4e-11:285:67//AC003694

R-HEMBA1002039

R-HEMBA1002049//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING DRAFT SEQUENCE.//5.3e-52:266:84//AL022315

R-HEMBA1002084//CIT-HSP-2357L11.TR CIT-HSP Homo sapiens genomic clone 23 57L11, genomic survey sequence.//0.0013:185:66//AQ063078

R-HEMBA1002092//Mus musculus 01f-1/EBF-like-3 transcription factor (0/E-3) mRNA, complete cds.//2.7e-70:479:86//U92703

R-HEMBA1002100//Homo sapiens thyroid receptor interactor (TRIP7) mRNA, 3' end of cds.//8.5e-32:206:91//L40357

R-HEMBA1002102//Homo sapiens Chromosome 15q26.1 PAC clone pDJ427d15, complete sequence.//4.3e-42:302:85//AC005800

R-HEMBA1002113//Human chromosome 12p13 sequence, complete sequence.//1.6e-64:550:80//U47924

R-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.2e-92:435:92//AC000378

R-HEMBA1002125

R-HEMBA1002139//Human nebulin mRNA, partial cds.//0.056:68:88//U35637

R-HEMBA1002144//Homo sapiens Chromosome 11p14.3 PAC clone 6-130a9 containing tryptophan hydroxylase gene, complete sequence.//2.0e-26:323:70//AC005728